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OM protein - protein search, using sw model

Run on: April 2, 2003, 14:27:44 ; Search time 72 Seconds
(without alignments)
198.025 Million cell updates/sec

Title: US-09-875-221B-9

Perfect score: 559
Sequence: 1 DIQMTPSPSLSSASVGDRTV.....CQGYNIYPLFFGGTKEIK 107

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	559	100.0	107	23	AAE19664	Human TNF40-g11 CD
2	559	100.0	214	23	AAE19666	Antibody Fab and m
3	554	99.1	107	23	AAE19665	Human TNF40-g12 CD
4	520	93.0	107	21	AAV56680	Anti-erythropoietin
5	513	91.8	126	17	AAW04387	Chimaeric human/mu
6	509	91.1	126	16	AAW04388	Human/murine chime
7	509	91.1	126	16	AAW04389	Human/murine chime
8	509	91.1	126	17	AAW04390	Chimaeric human/mu
9	509	91.1	126	17	AAW04395	Chimaeric human/mu
10	509	91.1	269	16	AAW04396	Human ONS-W21 anti

11	509	91.1	269	17	AAW04397	Chimaeric human/mu
12	506	90.5	126	16	AAW04398	Human/murine chime
13	506	90.5	126	16	AAW04399	Chimaeric human/mu
14	505	90.3	126	16	AAW04400	Human/murine chime
15	505	90.3	126	16	AAW04401	Chimaeric human/mu
16	504	90.2	126	16	AAW04402	Human/murine chime
17	504	90.2	126	16	AAW04403	Chimaeric human/mu
18	504	90.2	126	16	AAW04404	Human/murine chime
19	504	90.2	126	17	AAW04405	Chimaeric human/mu
20	503	90.0	126	16	AAW04406	Human/murine chime
21	502	89.8	126	16	AAW04407	Human/murine chime
22	502	89.8	126	16	AAW04408	Chimaeric human/mu
23	502	89.8	126	16	AAW04409	Human/murine chime
24	502	89.8	126	17	AAW04410	Chimaeric human/mu
25	502	89.8	126	17	AAW04411	Human/murine chime
26	500	89.4	126	16	AAW04412	Chimaeric human/mu
27	500	89.4	126	17	AAW04413	Human/murine chime
28	498	89.1	126	16	AAW04414	Chimaeric human/mu
29	498	89.1	126	17	AAW04415	Human/murine chime
30	497.5	89.0	109	16	AAW04416	Chimaeric human/mu
31	497	88.9	102	21	AAW04417	Humanized 3G9 high
32	497	88.9	107	22	AAW04418	Humanized Fab vers
33	497	88.9	107	22	AAW04419	Humanized anti-Erb
34	497	88.9	107	22	AAW04420	Humanized Fab vers
35	497	88.9	108	21	AAW04421	Erythropoietin rec
36	497	88.9	109	23	AAW04422	Human antibody 574
37	497	88.9	126	16	AAW04423	Human/murine chime
38	497	88.9	126	17	AAW04424	Chimaeric human/mu
39	497	88.9	126	16	AAW04425	Human/murine chime
40	494	88.4	126	16	AAW04426	Human/murine chime
41	493	88.2	108	21	AAW04427	Erythropoietin rec
42	492	88.0	126	16	AAW04428	Human/murine chime
43	491	87.8	108	21	AAW04429	Erythropoietin rec
44	491	87.8	126	16	AAW04430	Human/murine chime
45	491	87.8	126	17	AAW04431	Chimaeric human/mu

ALIGNMENTS

RESULT 1	AAE19664	standard; Protein: 107 AA.
XX	AAE19664;	
AC	AAE19664;	
XX		
DT	31-MAY-2002 (first entry)	
XX		
DE	Human TNF40-g11 CDR grafted variable light chain (VL) protein.	
XX		
KW	Human: tumour necrosis factor 40; TNF40; osteopathic; cardiant; CDR:	
KW	complementarity determining region; rheumatoid; osteo-arthritis; sepsis;	
KW	congestive heart failure; shock; tissue transplant; tuberculosis; AIDS;	
KW	Acquired Immune Deficiency Syndrome; adult respiratory distress syndrome;	
KW	chlexia; allergy; psoriasis; blood coagulation disorder; thyroiditis;	
KW	inflammatory bone disorder; Crohn's disease; autoimmune disease; burn;	
KW	neoplasia therapy; immunomodulator; vulnary; graft rejection.	
XX		
OS	Homo sapiens.	
PN	WO200194585-A1.	
PD	13-DEC-2001.	
XX		
XX	05-JUN-2001; 2001WO-GB02477.	
PR	06-JUN-2000; 2000GB-0013810.	
XX		
PA	(CELL-) CELTECH R & D LTD.	
XX		
PI	Athwal DS, Brown DT, Weir ANC, Poplewell AG, Chapman AP, King DT;	
XX		
DR	WPI; 2002-216732/27.	

DR N-PSDB; AAD31279.

XX New antibody specific for human tumor necrosis factor (TNF)-alpha,
 PT useful for treating TNF-alpha-mediated diseases, e.g. congestive heart
 PT failure, septic or endotoxic shock, cachexia, adult respiratory
 PT distress syndrome -

XX
 PS Claim 12; Fig 8; 119pp; English.

XX The invention relates to an antibody molecule having specificity for
 CC human tumor necrosis factor-alpha (TNFalpha) comprising a heavy or light
 CC chain. The antibody or the compound comprising the antibody is useful
 CC for treating or manufacturing a medicament for treating a pathology
 CC mediated by TNFalpha, such as rheumatoid or osteo-arthritis. TNFalpha
 CC mediated diseases which can be treated by the antibody include sepsis,
 CC congestive heart failure, septic or endotoxic shock, cachexia, adult
 CC respiratory distress syndrome, acquired immunodeficiency syndrome (AIDS),
 CC allergies, psoriasis, tuberculosis, inflammatory bone disorders, blood
 CC coagulation disorders, burns, rejection episodes following organ or
 CC tissue transplant, Crohn's disease and autoimmune diseases, such as
 CC thyroiditis. The antibodies may also be used to reduce the side effects
 CC associated with TNFalpha generation during neoplasia therapy, to
 CC eliminate or reduce shock-related symptoms associated with the treatment
 CC or prevention of graft rejection by use of an anti-lymphocyte antibody,
 CC for treating multi-organ failure, or in the diagnosis and imaging of
 CC disease states involving elevated levels of TNF alpha. The present
 CC sequence is complementarily determining (CDR) grafted light chain human
 CC tumour necrosis factor (TNF) 40-gL1 protein.

XX
 SQ Sequence 107 AA;

Query Match 100.0%; Score 559; DB 23; Length 107;
 Best Local Similarity 100.0%; Pred. No. 7.7e-35;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMOSPSSLSASVGDRTITCKASQNGTNVAMWQKRGKAPKALISASFLYSGVY 60
 Db 1 DIQMOSPSSLSASVGDRTITCKASQNGTNVAMWQKRGKAPKALISASFLYSGVY 60

QY 61 RFSGSGSGTDFLTITSSLOPEDFATYYCOQYNIYPLTFGQGRKVEIK 107
 Db 61 RFSGSGSGTDFLTITSSLOPEDFATYYCOQYNIYPLTFGQGRKVEIK 107

RESULT 2
 AAE19696
 ID AAE19696 standard; Protein; 214 AA.

XX
 AC AAE19696;

XX
 DT 31-MAY-2002 (first entry)

XX
 DE Antibody Fab and modified Fab fragment grafted light chain protein.

XX
 KM Tumour necrosis factor 40; TNF40; osteopathic; cardiant; vulnerrary; CDR;
 KM complementarity determining region; rheumatoid; osteo-arthritis; sepsis;
 KM congestive heart failure; shock; tissue transplant; tuberculosis; AIDS;
 KM Acquired Immune Deficiency Syndrome; adult respiratory distress syndrome;
 KM cachexia; allergy; psoriasis; blood coagulation disorder; thyroiditis;
 KM inflammatory bone disorder; Crohn's disease; autoimmune disease; burn;
 KM neoplasia therapy; immunomodulator; graft rejection; antibody.

XX
 OS Unidentified.

XX
 PN WO200194585-A1.

XX
 PD 13-DEC-2001.

XX
 PF 05-JUN-2001; 2001WO-GB02477.

XX
 PR 06-JUN-2000; 2000GB-0013810.

XX
 PA (CELL-) CELLTech R & D LTD.

XX
 PI Athwal DS, Brown DT, Weir AMC, Popplewell AG, Chapman AP, King DJ;
 XX WPI; 2002-216732/27.
 DR N-PSDB; AAD31362.

XX
 PS Claim 14; Page 113-114; 119pp; English.

XX The invention relates to an antibody molecule having specificity for
 CC human tumor necrosis factor-alpha (TNFalpha) comprising a heavy or light
 CC chain. The antibody or the compound comprising the antibody is useful
 CC for treating or manufacturing a medicament for treating a pathology
 CC mediated by TNFalpha, such as rheumatoid or osteo-arthritis. TNFalpha
 CC mediated diseases which can be treated by the antibody include sepsis,
 CC congestive heart failure, septic or endotoxic shock, cachexia, adult
 CC respiratory distress syndrome, acquired immunodeficiency syndrome (AIDS),
 CC allergies, psoriasis, tuberculosis, inflammatory bone disorders, blood
 CC coagulation disorders, burns, rejection episodes following organ or
 CC tissue transplant, Crohn's disease and autoimmune diseases, such as
 CC thyroiditis. The antibodies may also be used to reduce the side effects
 CC associated with TNFalpha generation during neoplasia therapy, to
 CC eliminate or reduce shock-related symptoms associated with the treatment
 CC or prevention of graft rejection by use of an anti-lymphocyte antibody,
 CC for treating multi-organ failure, or in the diagnosis and imaging of
 CC disease states involving elevated levels of TNF alpha. The present
 CC sequence is antibody Fab and modified Fab fragment grafted light chain
 CC used in the invention.

XX
 SQ Sequence 214 AA;

Query Match 100.0%; Score 559; DB 23; Length 214;
 Best Local Similarity 100.0%; Pred. No. 1.4e-34;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMOSPSSLSASVGDRTITCKASQNGTNVAMWQKRGKAPKALISASFLYSGVY 60
 Db 1 DIQMOSPSSLSASVGDRTITCKASQNGTNVAMWQKRGKAPKALISASFLYSGVY 60

QY 61 RFSGSGSGTDFLTITSSLOPEDFATYYCOQYNIYPLTFGQGRKVEIK 107
 Db 61 RFSGSGSGTDFLTITSSLOPEDFATYYCOQYNIYPLTFGQGRKVEIK 107

RESULT 3
 AAE19665
 ID AAE19665 standard; Protein; 107 AA.

XX
 AC AAE19665;

XX
 DT 31-MAY-2002 (first entry)

XX
 DE Human TNF40-gL2 CDR grafted variable light chain (VL) protein.

XX
 KM Human; tumour necrosis factor 40; TNF40; osteopathic; cardiant; CDR;
 KM complementarity determining region; rheumatoid; osteo-arthritis; sepsis;
 KM congestive heart failure; shock; tissue transplant; tuberculosis; AIDS;
 KM Acquired Immune Deficiency Syndrome; adult respiratory distress syndrome;
 KM cachexia; allergy; psoriasis; blood coagulation disorder; thyroiditis;
 KM inflammatory bone disorder; Crohn's disease; autoimmune disease; burn;
 KM neoplasia therapy; immunomodulator; vulnerrary; graft rejection.

XX
 OS Homo sapiens.

XX
 PN WO200194585-A1.

XX
 PD 13-DEC-2001.

XX
 PF 05-JUN-2001; 2001WO-GB02477.

XX 06-JUN-2000; 2000GB-0013810.
 PR (CELL-) CELTECH R & D LTD.
 XX Athwal DS, Brown DT, Weir ANC, Poplewell AG, Chapman AP, King DJ;
 XX WPI: 2002-216732/27.
 DR N-PSDB; AAD31280.
 XX New antibody specific for human tumor necrosis factor (TNF)-alpha,
 PT useful for treating TNF-alpha-mediated diseases, e.g. congestive heart
 PT failure, septic or endotoxemic shock, cachexia, adult respiratory
 PT distress syndrome -
 XX Example 1; Fig 9; 119pp; English.
 PS
 XX The invention relates to an antibody molecule having specificity for
 CC human tumor necrosis factor-alpha (TNFalpha) comprising a heavy or light
 CC chain. The antibody or the compound comprising the antibody is useful
 CC for treating or manufacturing a medicament for treating a pathology
 CC mediated by TNFalpha, such as rheumatoid or osteo-arthritis. TNFalpha
 CC mediated diseases which can be treated by the antibody include sepsis,
 CC congestive heart failure, septic or endotoxemic shock, cachexia, adult
 CC respiratory distress syndrome, acquired immunodeficiency syndrome (AIDS),
 CC allergies, psoriasis, tuberculosis, inflammatory bone disorders, blood
 CC coagulation disorders, burns, rejection episodes following organ or
 CC tissue transplant, Crohn's disease and autoimmune diseases, such as
 CC thyroiditis. The antibodies may also be used to reduce the side effects
 CC associated with TNFalpha generation during neoplasia therapy, to
 CC eliminate or reduce shock-related symptoms associated with the treatment
 CC or prevention of graft rejection by use of an anti-lymphocyte antibody,
 CC for treating multi-organ failure, or in the diagnosis and imaging of
 CC disease states involving elevated levels of TNF alpha. The present
 CC sequence is complementarily determining (CDR) grafted light human
 CC tumour necrosis factor (TNF) 40-gL2 protein.
 XX
 SQ Sequence 107 AA;
 Query Match 99.1%; Score 554; DB 23; Length 107;
 Best Local Similarity 99.1%; Pred. No. 1.8e-34;
 Matches 106; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DIQMTQSPSSLSASVGRVITTCASQNVGTNVAWYQOKPEKAKALYSASFISGVPY 60
 DB 1 DIQMTQSPSSLSASVGRVITTCASQNVGTNVAWYQOKPEKAKALYSASFISGVPY 60
 QY 61 RFGSGSGGTDFTLTITSLQPEDFATYYCOQYNIPLTFGGGTKEIK 107
 DB 61 RFGSGSGGTDFTLTITSLQPEDFATYYCOQYNIPLTFGGGTKEIK 107
 RESULT 4
 AAY56680
 ID AAY56680 standard; protein; 107 AA.
 AC AAY56680;
 XX
 DT 15-FEB-2000 (first entry)
 XX
 DE Anti-erythropoietin receptor Mab 3G9 light chain variable region.
 XX
 KW Complementarity determining region; antibody; immunogenicity;
 KW Old World ape; Old World monkey; antigen-binding affinity.
 XX
 OS Synthetic.
 OS Mus sp.
 XX Pan troglodytes.
 XX
 PN WO955369-A1.
 XX
 PD 04-NOV-1999.
 XX

PF 28-APR-1999; 99WO-US09131.
 XX
 PR 28-APR-1998; 98US-0083367.
 XX
 PA (SMIR) SMITHKLINE BEECHAM CORP.
 XX
 PI Taylor AH;
 XX
 DR WPI: 2000-023265/02.
 XX
 XX Antibodies containing donor complementarity determining regions and
 PT non-human primate acceptor frameworks, having reduced immunogenicity in
 PT humans -
 XX
 PS Example 8; Page 114-115; 123pp; English.
 XX
 XX The invention provides an antibody (Ab) comprising donor CDRs
 CC (complementarity determining regions) derived from a non-human antigen-
 CC specific donor antibody, and an acceptor framework from a non-human
 CC primate. The Abs are prepared by grafting CDRs from a non-human antigen-
 CC specific donor antibody onto homologous Old World ape or monkey acceptor
 CC frameworks. The Abs have reduced immunogenicity and are better tolerated
 CC in humans (because of the close similarity between the human and primate
 CC proteins), but retain the full antigen-binding affinity of the donor
 CC antibody.
 XX
 SQ Sequence 107 AA;
 Query Match 93.0%; Score 520; DB 21; Length 107;
 Best Local Similarity 94.4%; Pred. No. 6.2e-32;
 Matches 101; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 QY 1 DIQMTQSPSSLSASVGRVITTCASQNVGTNVAWYQOKPEKAKALYSASFISGVPY 60
 DB 1 DIQMTQSPSSLSASVGRVITTCASQNVGTNVAWYQOKPEKAKALYSASFISGVPY 60
 QY 61 RFGSGSGGTDFTLTITSLQPEDFATYYCOQYNIPLTFGGGTKEIK 107
 DB 61 RFGSGSGGTDFTLTITSLQPEDFATYYCOQYNIPLTFGGGTKEIK 107
 RESULT 5
 AAM04387
 ID AAM04387 standard; Protein; 126 AA.
 AC AAM04387;
 XX
 DT 09-DEC-1996 (first entry)
 XX
 DE Chimeric human/murine Mab ONS-M21 fragment HEF-RVL-M21b-g(kappa).
 XX
 KW Murine; human; myeloblastoma; chimeric; monoclonal antibody;
 KW chimera; single stranded Fv region; low human antigenicity;
 KW diagnosis; treatment; cerebral tumour; reshaped.
 XX
 OS Synthetic.
 XX
 FH Key
 FH Peptide
 FT 1..19
 FT /label= sig-peptide
 FT 20..125
 FT /label= mat-peptide
 FT 33..53
 FT /label= CDR_1
 FT 69..75
 FT /label= CDR_2
 FT 108..116
 FT /label= CDR_3
 XX
 XX Region
 XX
 XX JP08169900-A.
 XX
 PN 02-JUL-1996.
 XX
 PD
 XX

PF 18-NOV-1994; 94JP-0285057.
XX
PR 18-OCT-1994; 94JP-0252166.
XX 19-NOV-1993; 93JP-0291078.
XX
PA (CHUS) CHUGAI PHARM CO LTD.
XX
DR WPI; 1996-358509/36.
XX N-PSDB; AAT38628.
XX
PT Reshaped anti-human myeloblastoma cell human antibody - has low
PT human antigenicity, and is therefore useful for diagnosis and
PT treatment of cerebral tumours, e.g. myeloblastoma
XX
PS Example 5; Page 30; 45pp; Japanese.
XX
CC The present sequence is a fragment of the chimaeric human/murine
CC monoclonal antibody (Mab) ONS-M21. The Mab was prepd. by
CC combining light and heavy variable region DNA, from a murine
CC anti-human myeloblastoma cell Mab, with human light and heavy
CC constant region sequences, respectively to produce chimaeric
CC human/murine light and heavy chain DNA mols.. A recombinant vector
CC for the expression of the heavy and light chain DNA mols. was
CC prepd., and used to transform a host cell. The host cell was then
CC cultured, and the expression prods. of the heavy and light chain
CC DNA mols. sepd. and connected with a peptide linker to produce a
CC single stranded Fv region. The reshaped Fv region has low human
CC antigenicity, and is therefore expected to be useful as an agent
CC for the diagnosis and treatment of cerebral tumours,
CC e.g. myeloblastoma.
XX
SQ Sequence 126 AA:

Query Match 91.8%; Score 513; DB 17; Length 126;
Best Local Similarity 92.5%; Pred. No. 2.4e-31;
Matches 99; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTYITCKASQNVGTVMVYQOKPGKAPKALITYSASFLYSGVPY 60
DB 20 DIQMTQSPSSLSASVGDRTYITCKASQNVGTVMVYQOKPGKAPKALITYSASYRSGVPS 79
QY 61 RPSGSGSGDTFTLTISLQPEDFATYVCOQYNIVPLTFGSGGKVEIK 107
DB 80 RPSGSGSGDTFTLTISLQPEDIATYVCOQYNISPRAFGQGTKEIK 126

RESULT 6
AAR76680
ID AAR76680 standard; Protein: 126 AA.
XX
AC AAR76680;
XX
DT 17-JAN-1996 (first entry)
XX
DE Human/murine chimeric antibody HEF-RVL-M21p-g kappa.
XX
KW Human; murine; chimeric antibody; HEF-RVL-M21p-g kappa;
KW medulloblastoma; brain tumour; treatment; diagnosis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT /label= sig-peptide
FT 20..43
FT /label= FR 1
FT 44..54
FT /label= CDR 1
FT 55..69
FT /label= FR 2
FT 70..76
FT /label= CDR 2
FT 77..108
FT Peptide

FT /label= FR 3
FT Peptide 109..117
FT /label= CDR 3
FT Peptide 118..126
FT /label= FR 4

PN W09514041-A1.
XX
PD 26-MAY-1995.
XX
PF 19-OCT-1994; 94WO-JP01763.
XX
PR 19-NOV-1993; 93JP-0291078.
XX
PA (CHUS) CHUGAI SEIRYAKU KK.
XX
PI Ohmoto T, Sato K, Tsuchiya M;
XX WPI; 1995-200347/26.
DR N-PSDB; AAO94532.
XX
DR Reconstituted antibody against human medullo:blastoma cells -
XX contains high proportion of human antibody origin and has low
XX antigenicity
XX
PS Claim 24; Pages 90-91; 120pp; Japanese.
XX
CC AA094532 encodes AAR76680 the human/murine chimeric antibody HEF-
CC RVL-M21p-g kappa. The antibody is reactive with human medullo-
CC blastoma (a brain tumour) cells. The chimeric antibody can be
CC used in the diagnosis and treatment of this disease.
XX
SQ Sequence 126 AA:

Query Match 91.1%; Score 509; DB 16; Length 126;
Best Local Similarity 91.6%; Pred. No. 4.7e-31;
Matches 98; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTYITCKASQNVGTVMVYQOKPGKAPKALITYSASFLYSGVPY 60
DB 20 DIQMTQSPSSLSASVGDRTYITCKASQNVGTVMVYQOKPGKAPKALITYSASYRSGVPS 79
QY 61 RPSGSGSGDTFTLTISLQPEDFATYVCOQYNIVPLTFGSGGKVEIK 107
DB 80 RPSGSGSGDTFTLTISLQPEDIATYVCOQYNISPRAFGQGTKEIK 126

RESULT 7
AAR76665
ID AAR76665 standard; Protein: 126 AA.
XX
AC AAR76665;
XX
DT 17-JAN-1996 (first entry)
XX
DE Human/murine chimeric antibody HEF-RVL-M21a-g kappa.
XX
KW Human; murine; chimeric antibody; HEF-RVL-M21a-g kappa;
KW medulloblastoma; brain tumour; treatment; diagnosis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT /label= sig-peptide
FT 20..43
FT /label= FR 1
FT 44..54
FT /label= CDR 1
FT 55..69
FT /label= FR 2
FT 70..76
FT /label= CDR 2
FT 77..108
FT Peptide

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FT Peptide 77..108
FT /label= FR 3
FT Peptide 109..117
FT /label= CDR 3
FT Peptide 118..126
FT /label= FR 4
XX
XX WO9514041-A1.
XX
XX 26-MAY-1995.
XX
XX 19-OCT-1994; 94WO-JP01763.
XX
XX 19-NOV-1993; 93JP-0291078.
XX
XX (CHUS ) CHUGAI SEIYAKU KK.
XX
XX Ontomo T, Sato K, Tsuchiya M;
XX
XX WPI: 1995-200347/26.
XX
XX N-PSDB: AAQ94499.
XX
XX Reconstituted antibody against human medullo:blastoma cells -
XX contains high proportion of human antibody origin and has low
XX antigenicity
XX
XX Claim 33; Page 64; 120pp; Japanese.
XX
XX AAQ94499 encodes AAR7665 the human/murine chimeric antibody HEF-
XX RVL-W21a-g kappa. The antibody is reactive with human medullo-
XX blastoma (a brain tumour) cells. The chimeric antibody can be
XX used in the diagnosis and treatment of this disease.
XX
XX Sequence 126 AA;
XX
XX Query Match 91.1%; Score 509; DB 16; Length 126;
XX Best Local Similarity 91.6%; Pred. No. 4.7e-31;
XX Matches 98; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

OY 1 DIQMTQSPSSLSASVGRVTTTCRASQNVGNVAMVYQOKPGKAPKALITYSASYSGVPY 60
DB 20 DIQMTQSPSSLSASVGRVTTTCRASQNVGNVAMVYQOKPGKAPKALITYSASYSGVPS 79
OY 61 RFSGSGSTDEFTLTISLQPEDFATYYCOQYNIVPLTFGQGTKEIK 107
DB 80 RFSGSGSTDEFTLTISLQPEDFATYYCOQYNIVPLTFGQGTKEIK 126

RESULT 8
AAW04380
ID AAW04380 standard; Protein: 126 AA.
XX
XX AAW04380;
XX
XX 09-DEC-1996 (first entry)
XX
XX Chimaeric human/murine MAb ONS-M21 fragment HEF-RVL-W21a-g(kappa).
XX
XX Murine: human; myeloblastoma; chimaera; monoclonal antibody;
XX chimaera; single stranded Fv region; low human antigenicity;
XX diagnosis; treatment; cerebral tumour; reshaped.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Peptide 1..19
XX /label= sig_peptide
XX 20..125
XX /label= mat_peptide
XX 33..53
XX /label= CDR_1
XX 69..75
XX /label= CDR_2
XX
XX Region
XX
XX Peptide

```

```

FT Region 108..116
FT /label= CDR_3
XX
XX JP08169900-A.
XX
XX 02-JUL-1996.
XX
XX 18-NOV-1994; 94JP-0285057.
XX
XX 18-OCT-1994; 94JP-0252166.
XX
XX 19-NOV-1993; 93JP-0291078.
XX
XX (CHUS ) CHUGAI PHARM CO LTD.
XX
XX WPI: 1996-358509/36.
XX
XX N-PSDB: AAT38613.
XX
XX Reshaped anti-human myeloblastoma cell human antibody - has low
XX human antigenicity, and is therefore useful for diagnosis and
XX treatment of cerebral tumours, e.g. myeloblastoma
XX
XX Example 5; Page 24; 45pp; Japanese.
XX
XX The present sequence is a fragment of the chimaeric human/murine
XX monoclonal antibody (MAb) ONS-M21. The MAb was prep'd. by
XX combining light and heavy variable region DNA, from a murine
XX anti-human myeloblastoma cell MAb, with human light and heavy
XX constant region sequences, respectively to produce chimaeric
XX human/murine light and heavy chain DNA mols.. A recombinant vector
XX for the expression of the heavy and light chain DNA mols. was
XX prep'd., and used to transform a host cell. The host cell was then
XX cultured, and the expression prods. of the heavy and light chain
XX DNA mols. sepd. and connected with a peptide linker to produce a
XX single stranded Fv region. The reshaped Fv region has low human
XX antigenicity, and is therefore expected to be useful as an agent
XX e.g. myeloblastoma.
XX
XX Sequence 126 AA;
XX
XX Query Match 91.1%; Score 509; DB 17; Length 126;
XX Best Local Similarity 91.6%; Pred. No. 4.7e-31;
XX Matches 98; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

OY 1 DIQMTQSPSSLSASVGRVTTTCRASQNVGNVAMVYQOKPGKAPKALITYSASYSGVPY 60
DB 20 DIQMTQSPSSLSASVGRVTTTCRASQNVGNVAMVYQOKPGKAPKALITYSASYSGVPS 79
OY 61 RFSGSGSTDEFTLTISLQPEDFATYYCOQYNIVPLTFGQGTKEIK 107
DB 80 RFSGSGSTDEFTLTISLQPEDFATYYCOQYNIVPLTFGQGTKEIK 126

RESULT 9
AAW04395
ID AAW04395 standard; Protein: 126 AA.
XX
XX AAW04395;
XX
XX 09-DEC-1996 (first entry)
XX
XX Chimaeric human/murine MAb ONS-M21 fragment HEF-RVL-W21p-g(kappa).
XX
XX Murine: human; myeloblastoma; chimaera; monoclonal antibody;
XX chimaera; single stranded Fv region; low human antigenicity;
XX diagnosis; treatment; cerebral tumour; reshaped.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Peptide 1..19
XX /label= sig_peptide
XX 20..125
XX
XX Region
XX
XX Peptide

```

```

FT      Region          /label= mat_peptide
FT      33..53         /label= CDR_1
FT      Region          /label= CDR_1
FT      69..75         /label= CDR_2
FT      Region          /label= CDR_2
FT      108..116       /label= CDR_3
FT      JP08169900-A.
PA      02-JUL-1996.
PD      18-NOV-1994;   94JP-0285057.
PF      18-NOV-1994;   94JP-0252166.
PR      19-NOV-1993;    93JP-0291078.
XX      (CHUS ) CHUGAI PHARM CO LTD.
XX      WPI; 1996-358509/36.
XX      N-PSTDB; AAT38646.
XX      Reshaped anti-human myeloblastoma cell human antibody - has low
PT      human antigenicity, and is therefore useful for diagnosis and
PT      treatment of cerebral tumours, e.g. myeloblastoma
XX      Example 5; Page 37; 45pp; Japanese.
XX      The present sequence is a fragment of the chimaeric human/murine
CC      monoclonal antibody (Mab) ONS-M21. The Mab was prepd. by
CC      combining light and heavy variable region DNA, from a murine
CC      anti-human myeloblastoma cell Mab, with human light and heavy
CC      constant region sequences, respectively to produce chimaeric
CC      human/murine light and heavy chain DNA mols.. A recombinant vector
CC      for the expression of the heavy and light chain DNA mols. was
CC      prepd., and used to transform a host cell. The host cell was then
CC      cultured, and the expression prods. of the heavy and light chain
CC      DNA mols. sepd. and connected with a peptide linker to produce a
CC      single stranded Fv region. The reshaped Fv region has low human
CC      antigenicity, and is therefore expected to be useful as an agent
CC      for the diagnosis and treatment of cerebral tumours,
CC      e.g. myeloblastoma.
SO      Sequence      126 AA;
OY      Query Match           91.1%; Score 509; DB 17; Length 126;
OY      Best Local Similarity 91.6%; Pred. No. 4,7e-31;
Db      Matches 98; Conservative 1; Mismatches 8; Indels 0; Gaps 0
OY      1 DIQMQRPSLSASVGDRITTCCKASQNVGVNVMYQKPGAKPLITSASLTSGVRY 60
OY      |IIIIII|PSSLSASVGDRITTCCKASQNVGVNVMYQKPGAKPLITSASLTSGVRY 60
OY      20 DIQMQRSPSSLSASVGDRITTCCKASQNVGVNVMYQKPGAKPLIYSASYSRGVPS 79
OY      61 RFSGGSGGDFELTISLDPEDFAHYCYCOQYNINYLPLEFGGGRKVEIK 107
OY      |||||IIIIII|IIIIII|IIIIII|IIIIII|IIIIII|IIIIII|IIIIII|IIIIII|
OY      80 RFSGGSGGDFELTISLDPEDIAITYCYCOQYNINYPRAFGGGRKVEIK 126
RESULT 10
ID      AAR76682
XX      AAR76682 standard: Protein; 269 AA.
XX      AAR76682;
XX      18-JAN-1996 (first entry)
XX      Human ONS-M21 antibody Fv fragment.
XX      Plasmid pSCFYT7-IM21; human; ONS-M21 antibody; chimeric protein;
KW      medulloblastoma; brain tumour; treatment; diagnosis; Fv fragment.
XX      Homo sapiens.
XX
```

FH	Key		Location/Qualifiers
FT	Peptide	1..22	
FT	Region	23..139	/label= "sig-peptide"
FT	Region	140..154	/note= "heavy variable region"
FT	Region	155..269	/note= "linker"
FT	Region	262..269	/note= "light variable region"
FT	Region		/note= "FLAG"
XX			
XX			
PN	WO9514041-A1.		
PD	26-MAY-1995.		
XX			
PF	19-OCT-1994;	94WO-JP01763.	
XX			
PR	19-NOV-1993;	93JP-0291078.	
XX			
PA	(CHUS) CHUGAI SEIYAKU KK.		
PI	Ohtomo T, Sato K, Tsuchiya M;		
DR	WPI; 1995-200347/26.		
DR	N-PSTB; AA094548.		
XX			
PT	Reconstituted antibody against human medulloblastoma cells -		
PT	contains high proportion of human antibody origin and has low		
PT	antigenicity		
PS	Claim 35; Pages 98-99; 120pp; Japanese.		
CC			
CC	AA094548 is the plasmid pSCFVT7-hM21, which encodes AAR76682 the		
CC	human antibody ONS-W21 Fv fragment. The plasmid was used in the		
CC	construction of an expression vector. contg. cDNA encoding a		
CC	human/murine chimeric antibody, reactive with human medullo-		
CC	blastoma (a brain tumour) cells. The chimeric antibody can be		
CC	used in the diagnosis and treatment of this disease.		
SQ	Sequence 269 AA:		
Query Match	91.1%; Score 509; DB 16; Length 269;		
Best Local Similarity	91.6%; Pred. No. 9.3e-31;		
Matches 98; Conservative 1; Mismatches 8; Indels 0; Gaps 0,			
QY	1 DIQMOTSPSSLSASGVDRYTITCKASQNVTNVAWTQQKPGKAPRALYSASFLYSGVPY 60 155 DIQMTGSPSSLASAGDKRVTITCKASKSNVGTNVAMTQQKPGKAPRLIYSASYRGVS 214 		
DY	61 RFSSGSGETDFTLTTLTSLOPEDPATYYCOQNYIVPLTFEGQTKEIK 107 215 RFSGGSGTGDFETFTISLQPEDIATYYCOQNYSPRAFQGKTKEIK 261 		
RESULT 11			
AAW04397			
ID	AAW04397 standard; Protein: 269 AA.		
XX			
AC	AAW04397;		
DT	09-DEC-1996 (first entry)		
DE	Chimaeric human/murine Mab ONS-W21 scfv fragment.		
KW	Murine; human; myeloblastoma; chimera; monoclonal antibody;		
KW	chimera; single stranded Fv region; low human antigenicity;		
KW	diagnosis; treatment; cerebral tumour; reshaped.		
OS	Synthetic.		
TH	Key	Location/Qualifiers	
FT	Peptide	1..22	

```

FT      Region      /label= sig_peptide
FT      23..139
FT      /note= "heavy variable region"
FT      Peptide      140..154
FT      /label= linker
FT      Region      155..261
FT      /note= "light variable region"
FT      Peptide      262..269
FT      /label= FLAG
PN      JP08169900-A.
XX
XX      02-JUL-1996.
XX
XX      18-NOV-1994; 94JP-0285057.
XX
XX      18-OCT-1994; 94JP-0252166.
XX      19-NOV-1993; 93JP-0291078.
XX
XX      (CHUS ) CHUGAI PHARM CO LTD.
XX
XX      WPI; 1996-358509/36.
XX      N-PSDB; AAT38662.
XX
XX      Reshaped anti-human myeloblastoma cell human antibody - has low
XX      human antigenicity, and is therefore useful for diagnosis and
XX      treatment of cerebral tumours, e.g. myeloblastoma
XX
XX      Example 6; Pages 40-41; 45pp; Japanese.
XX
XX      The present sequence is a scfv fragment from the chimaeric
XX      human/murine monoclonal antibody (Mab) ONS-M21. The Mab was
XX      prepared by combining light and heavy variable region DNA from a
XX      murine anti-human myeloblastoma cell Mab, with human light and
XX      heavy constant region sequences, respectively to produce chimeric
XX      human/murine light and heavy chain DNA mols. A recombinant vector
XX      for the expression of the heavy and light chain DNA mols. was
XX      prepared, and used to transform a host cell. The host cell was then
XX      cultured, and the expression prods. of the heavy and light chain
XX      DNA mols. sepd. and connected with a peptide linker to produce a
XX      single stranded Fv region. The reshaped Fv region has low human
XX      antigenicity, and is therefore expected to be useful as an agent
XX      for the diagnosis and treatment of cerebral tumours,
XX      e.g. myeloblastoma.
XX
SQ      Sequence 269 AA:
Query Match 91.1%; Score 509; DB 17; Length 269;
Best Local Similarity 91.6%; Pred. No. 9.3e-31;
Matches 98; Conservative 1; Mismatches 8; Indels 0; Gaps 0;
OY      1 DIQMTQSPSSISASVGRVITTCASQNVGTVAMVYQOKPEKAPKALYLSFLYSGVPY 60
DB      155 DIQMTQSPSSISASVGRVITTCASQNVGTVAMVYQOKPEKAPKALYLSFLYSGVPS 214
OY      61 RFSGSGGTDFTLTSSLOPEDFATYVCOQYNYPLTFGGGTKEIK 107
DB      215 RFSGSGGTDFTLTSSLOPEDATYVCOQYNSYPRAFGGGTKEIK 261

```

RESULT 12
AAR76666
ID AAR76666 standard; Protein; 126 AA.

AC AAR76666;
XX
DT 17-JAN-1996 (first entry)
XX
DE Human/murine chimeric antibody HEF-RVL-M21b-g kappa.
XX
KW Human; murine; chimeric antibody; HEF-RVL-M21b-g kappa;
KW medulloblastoma; brain tumour; treatment; diagnosis.

```

OS      Homo sapiens.
XX
XX      Key      Location/Qualifiers
XX      Peptide 1..19
XX      /label= sig_peptide
XX      Peptide 20..43
XX      /label= FR 1
XX      Peptide 44..54
XX      /label= CDR 1
XX      Peptide 55..69
XX      /label= FR 2
XX      Peptide 70..76
XX      /label= CDR 2
XX      Peptide 77..108
XX      /label= FR 3
XX      Peptide 109..117
XX      /label= CDR 3
XX      Peptide 118..126
XX      /label= FR 4

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W09514041-A1.

XX 26-MAY-1995.

XX 19-OCT-1994; 94WO-JP01763.

XX 19-NOV-1993; 93JP-0291078.

XX (CHUS) CHUGAI SEIYAKU KK.

XX Ontomo T, Sato K, Tsuchiya M;

XX WPI; 1995-200347/26.

XX Reconstituted antibody against human medullo:blastoma cells -
XX contains high proportion of human antibody origin and has low
XX antigenicity

XX Claim 33; Page 66; 120pp; Japanese.

XX AA094502 encodes AAR76666 the human/murine chimeric antibody HEF-
XX RVL-M21b-g kappa. The antibody is reactive with human medullo-
XX blastoma (a brain tumour) cells. The chimeric antibody can be
XX used in the diagnosis and treatment of this disease.

XX Sequence 126 AA:

Query Match 90.5%; Score 506; DB 16; Length 126;
Best Local Similarity 90.7%; Pred. No. 7.9e-31;
Matches 97; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

OY 1 DIQMTQSPSSISASVGRVITTCASQNVGTVAMVYQOKPEKAPKALYLSFLYSGVPY 60
DB 20 DIQMTQSPSSISASVGRVITTCASQNVGTVAMVYQOKPEKAPKALYLSFLYSGVPS 79

OY 61 RFSGSGGTDFTLTSSLOPEDFATYVCOQYNYPLTFGGGTKEIK 107
DB 80 RFSGSGGTDFTLTSSLOPEDATYVCOQYNSYPRAFGGGTKEIK 126

RESULT 13
AAW04381
ID AAW04381 standard; Protein; 126 AA.

AC AAW04381;
XX
DT 09-DEC-1996 (first entry)
XX
DE Chimaeric human/murine Mab ONS-M21 fragment HEF-RVL-M21b-g(kappa).
XX
XX Murine; human; myeloblastoma; chimaera; monoclonal antibody;
KW chimaera; single stranded Fv region; low human antigenicity;
KW diagnosis; treatment; cerebral tumour; reshaped.

```

XX OS Synthetic.
XX Key Location/Qualifiers
FH Peptide 1..19
FT Peptide /label= sig_peptide
FT Peptide 20..125
FT Peptide /label= mat_peptide
FT Region 33..53
FT Region /label= CDR_1
FT Region 69..75
FT Region /label= CDR_2
FT Region 108..116
FT Region /label= CDR_3
PN JP08169900-A.
XX 02-JUL-1996.
XX 18-NOV-1994: 94JP-0285057.
XX 18-OCT-1994: 94JP-0252166.
XX 19-NOV-1993: 93JP-0291078.
XX (CHUS ) CHUGAI PHARM CO LTD.
XX WPI: 1996-358509/36.
XX N-PSDB: AAT38616.
XX
XX Reshaped anti-human myeloblastoma cell human antibody - has low
XX human antigenicity, and is therefore useful for diagnosis and
XX treatment of cerebral tumours, e.g. myeloblastoma
XX
XX Example 5: Page 25; 45pp; Japanese.
XX
CC The present sequence is a fragment of the chimaeric human/murine
CC monoclonal antibody (Mab) ONS-M21. The Mab was prepd. by
CC combining light and heavy variable region DNA, from a murine
CC anti-human myeloblastoma cell Mab, with human light and heavy
CC constant region sequences, respectively to produce chimaeric
CC human/murine light and heavy chain DNA mols.. A recombinant vector
CC for the expression of the heavy and light chain DNA mols. was
CC prepd., and used to transform a host cell. The host cell was then
CC cultured, and the expression prods. of the heavy and light chain
CC DNA mols. sep'd. and connected with a peptide linker to produce a
CC single stranded Fv region. The reshaped Fv region has low human
CC antigenicity, and is therefore expected to be useful as an agent
CC for the diagnosis and treatment of cerebral tumours,
CC e.g. myeloblastoma.
XX
SQ Sequence 126 AA:
Query Match 90.5%; Score 506; DB 17; Length 126;
Best Local Similarity 90.7%; Pred. No. 7.9e-31;
Matches 97; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
QY 1 DIOMTQSPSSLASVGDRTITCKASQNGTNVAMWQKPGKAPKALISASFLYSGVPY 60
DB 20 DIOMTQSPSSLASVGDRTITCKASQNGTNVAMWQKPGKAPKALISASFLYSGVPS 79
QY 61 RFGSGSGTDFLTITSSLOPEDFATYYCOQYNIYPLTFEGQTKVEIK 107
DB 80 RFGSGSGTDFLTITSSLOPEDFATYYCOQYNSYPRAFGQTKVEIK 126

```

RESULT 14

```

AAK76667
ID AAK76667 standard; Protein; 126 AA.
XX
AC AAK76667;
XX
DT 17-JAN-1996 (first entry)
XX

```

```

DE Human/murine chimeric antibody HEF-RVL-M21c-g kappa.
XX
XX Human; murine; chimeric antibody; HEF-RVL-M21c-g kappa;
KW medulloblastoma; brain tumour; treatment; diagnosis.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Peptide 1..19
FT Peptide /label= sig_peptide
FT Peptide 20..43
FT Peptide /label= FR 1
FT Peptide 44..54
FT Peptide /label= CDR 1
FT Peptide 55..69
FT Peptide /label= FR 2
FT Peptide 70..76
FT Peptide /label= CDR 2
FT Peptide 77..108
FT Peptide /label= FR 3
FT Peptide 109..117
FT Peptide /label= CDR 3
FT Peptide 118..126
FT Peptide /label= FR 4
PN WO9514041-A1.
XX 26-MAY-1995.
XX
XX 19-OCT-1994: 94WO-JP01763.
XX 19-NOV-1993: 93JP-0291078.
XX
XX (CHUS ) CHUGAI SEIYAKU KK.
XX
XX Ohtomo T, Sato K, Tsuchiya M;
XX WPI: 1995-200347/26.
XX N-PSDB: AA094505.
XX
XX Reconstituted antibody against human medulloblastoma cells -
XX contains high proportion of human antibody origin and has low
XX antigenicity
XX
XX Claim 33; Page 68; 120pp; Japanese.
XX
XX AA094505 encodes AAK76667 the human/murine chimeric antibody HEF-
XX RVL-M21c-g kappa. The antibody is reactive with human medullo-
XX blastoma (a brain tumour) cells. The chimeric antibody can be
XX used in the diagnosis and treatment of this disease.
XX
SQ Sequence 126 AA:
Query Match 90.3%; Score 505; DB 16; Length 126;
Best Local Similarity 90.7%; Pred. No. 9.4e-31;
Matches 97; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
QY 1 DIOMTQSPSSLASVGDRTITCKASQNGTNVAMWQKPGKAPKALISASFLYSGVPY 60
DB 20 DIOMTQSPSSLASVGDRTITCKASQNGTNVAMWQKPGKAPKALISASFLYSGVPS 79
QY 61 RFGSGSGTDFLTITSSLOPEDFATYYCOQYNIYPLTFEGQTKVEIK 107
DB 80 RFGSGSGTDFLTITSSLOPEDFATYYCOQYNSYPRAFGQTKVEIK 126

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RESULT 15

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AAW04382
ID AAW04382 standard; Protein; 126 AA.
XX
AC AAW04382;
XX
DT 09-DEC-1996 (first entry)
XX

```


XX Chimaeric human/murine MAb ONS-M21 fragment HEF-RVL-M21c-g(kappa).

DE Murine; human; myeloblastoma; chimaera; monoclonal antibody;
 XX chimaera; single stranded Fv region; low human antigenicity;
 KW diagnosis; treatment; cerebral tumour; reshaped.
 KW
 XX
 OS Synthetic.

XX
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT /label= sig_peptide
 FT 20..125
 FT /label= mat_peptide
 FT Region 33..53
 FT /label= CDR_1
 FT 69..75
 FT /label= CDR_2
 FT 108..116
 FT Region /label= CDR_3
 FT
 FT
 XX
 XX
 PN JP08169900-A.

XX
 PD 02-JUL-1996.
 XX
 PF 18-NOV-1994; 94JP-0285057.
 XX
 PR 18-OCT-1994; 94JP-0252166.
 PR 19-NOV-1993; 93JP-0291078.
 XX
 PA (CHUS) CHUGAI PHARM CO LTD.
 XX
 DR WPI: 1996-358509/36.
 DR N-PSDB: NAT38619.

XX Reshaped anti-human myeloblastoma cell human antibody - has low
 PT human antigenicity, and is therefore useful for diagnosis and
 PT treatment of cerebral tumours, e.g. myeloblastoma
 XX

PS Example 5; Page 26; 45pp; Japanese.

XX The present sequence is a fragment of the chimaeric human/murine
 CC monoclonal antibody (Mab) ONS-M21. The Mab was prepd. by
 CC combining light and heavy variable region DNA, from a murine
 CC anti-human myeloblastoma cell Mab, with human light and heavy
 CC constant region sequences, respectively to produce chimaeric
 CC human/murine light and heavy chain DNA mols.. A recombinant vector
 CC for the expression of the heavy and light chain DNA mols. was
 CC prepd., and used to transform a host cell. The host cell was then
 CC cultured, and the expression prods. of the heavy and light chain
 CC DNA mols. sepd. and connected with a peptide linker to produce a
 CC single stranded Fv region. The reshaped Fv region has low human
 CC antigenicity, and is therefore expected to be useful as an agent
 CC for the diagnosis and treatment of cerebral tumours,
 CC e.g. myeloblastoma.
 XX

SO Sequence 126 AA;

Query Match 90.3%; Score 505; DB 17; Length 126;
 Best Local Similarity 90.7%; Pred. No. 9.4e-31;
 Matches 97; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSSSSLSASVGDRTTICKASQNVGNVAVYQOKPGKAPKALISASFLYSGVPY 60
 DB 20 DIQMTQSSSSLSASVGDRTTICKASQNVGNVAVYQOKPGKAPKALISASRYSGVPS 79
 QY 61 RFGSGSGTDFLTITISLOPEDFATYCCQYNYIPLTFGQGTVEIK 107
 DB 80 RFGSGSGTDFLTITISLOPEDFATYCCQYNYIPLTFGQGTVEIK 126

Search completed: April 2, 2003, 14:37:06
 Job time : 73 secs

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GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: Apr11 2, 2003, 14:35:54 : Search time 28 Seconds
(without alignments)
112.438 Million cell updates/sec

Title: US-09-875-221b-9
Perfect score: 559
Sequence: 1 DIQMTQSPSSLSASVGRVT.....CQYNYVPLFRGQGRKVEIK 107

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Listing first 45 summaries

- Issued Patents_AA:*
- 1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
 - 2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
 - 3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
 - 4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
 - 5: /cgn2_6/ptodata/1/1aa/PCITUS.COMB.pep:*
 - 6: /cgn2_6/ptodata/1/1aa/backfill1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	513	91.8	126	4	US-08-646-265A-65
2	509	91.1	107	4	US-08-646-265A-130
3	509	91.1	126	4	US-08-646-265A-43
4	509	91.1	126	4	US-08-646-265A-91
5	509	91.1	269	4	US-08-646-265A-109
6	506	90.5	126	4	US-08-646-265A-47
7	505	90.3	126	4	US-08-646-265A-91
8	504	90.2	126	4	US-08-646-265A-57
9	504	90.2	126	4	US-08-646-265A-63
10	502	89.8	107	4	US-08-646-265A-131
11	502	89.8	126	4	US-08-646-265A-53
12	502	89.8	126	4	US-08-646-265A-85
13	502	89.8	126	4	US-08-646-265A-87
14	500	89.4	126	4	US-08-646-265A-75
15	498	89.1	126	4	US-08-646-265A-59
16	497.5	89.0	109	2	US-08-602-725-30
17	497	88.9	126	4	US-08-646-265A-69
18	497	88.9	126	4	US-08-646-265A-77
19	491	87.8	126	4	US-08-646-265A-73
20	490	87.7	126	1	US-08-202-047-13
21	490	87.7	126	1	US-08-202-047-15
22	490	87.7	126	3	US-08-964-690-13
23	490	87.7	126	3	US-08-964-690-15
24	486	86.9	126	1	US-08-202-047-17
25	486	86.9	126	1	US-08-202-047-19
26	486	86.9	126	3	US-08-964-690-17
27	486	86.9	126	3	US-08-964-690-19

28	484	86.6	126	4	US-08-646-265A-81	Sequence 81, Appl
29	481	86.0	107	2	US-07-934-373C-41	Sequence 41, Appl
30	481	86.0	107	3	US-08-437-642B-41	Sequence 41, Appl
31	481	86.0	214	4	US-09-679-397-1	Sequence 1, Appl1
32	481	86.0	214	4	US-09-680-148-1	Sequence 1, Appl1
33	481	86.0	237	2	US-08-463-587A-25	Sequence 25, Appl1
34	481	86.0	237	2	US-08-463-587A-3	Sequence 25, Appl1
35	481	86.0	237	3	US-08-923-854-25	Sequence 25, Appl1
36	481	86.0	237	5	PCT-US91-09133-26	Sequence 26, Appl
37	477	85.3	109	2	US-07-934-373C-3	Sequence 3, Appl1
38	477	85.3	109	3	US-08-437-642B-3	Sequence 3, Appl1
39	477	85.3	109	4	US-08-146-206C-3	Sequence 3, Appl1
40	477	85.3	109	5	PCT-US93-07832-3	Sequence 3, Appl1
41	476	85.2	108	3	US-08-974-899-2	Sequence 2, Appl1
42	474	84.8	107	2	US-07-934-373C-18	Sequence 18, Appl
43	474	84.8	107	2	US-07-934-373C-43	Sequence 43, Appl
44	474	84.8	107	3	US-08-437-642B-18	Sequence 18, Appl
45	474	84.8	107	3	US-08-437-642B-43	Sequence 43, Appl

ALIGNMENTS

RESULT 1
US-08-646-265A-65
Sequence 65, Application US/08646265A
Patent No. 6214973
GENERAL INFORMATION:
APPLICANT: OHTOMO, Toshihiko
APPLICANT: SATO, Koh
APPLICANT: TSUCHIYA, Masayuki
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: MEDULLOBLASTOMA CELLS
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,265A
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP94/01763
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-291078
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/184
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-646-265A-65
Query Match 91.8%; Score 513; DB 4; Length 126;

NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646, 265A
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP94/01763
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-291078
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/184
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-646-265A-91

Query Match 91.1%; Score 509; DB 4; Length 126;
Best Local Similarity 91.6%; Pred. No. 1.2e-40;
Matches 98; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 1 DIOMTQSPSSLSASVGDRTITCKASQNGTVAMVYQOKPGKAPRLIYSASFISGVY 60
Db 20 DIOMTQSPSSLSASVGDRTITCKASQNGTVAMVYQOKPGKAPRLIYSASFISGVPS 79

Qy 61 RFSGSGGTDFLTITSLQPEDFATYYCOQYNIYPLTFGQGTKEIK 107
Db 80 RFSGSGGTDFLTITSLQPEDIATYYCOQYNSYPRAFQGTKEIK 126

RESULT 5
US-08-646-265A-109
Sequence 109, Application US/08646265A
Patent No. 6214973
GENERAL INFORMATION:
APPLICANT: OHTOMO, Toshiniko
APPLICANT: SATO, Koh
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: MEDULLOBLASTOMA CELLS
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646, 265A
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP94/01763
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-291078
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/184
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 109:
SEQUENCE CHARACTERISTICS:
LENGTH: 269 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-646-265A-109

Query Match 91.1%; Score 509; DB 4; Length 269;
Best Local Similarity 91.6%; Pred. No. 2.8e-40;
Matches 98; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 1 DIOMTQSPSSLSASVGDRTITCKASQNGTVAMVYQOKPGKAPRLIYSASFISGVY 60
Db 155 DIOMTQSPSSLSASVGDRTITCKASQNGTVAMVYQOKPGKAPRLIYSASFISGVPS 214

Qy 61 RFSGSGGTDFLTITSLQPEDFATYYCOQYNIYPLTFGQGTKEIK 107
Db 215 RFSGSGGTDFLTITSLQPEDIATYYCOQYNSYPRAFQGTKEIK 261

RESULT 6
US-08-646-265A-47
Sequence 47, Application US/08646265A
Patent No. 6214973
GENERAL INFORMATION:
APPLICANT: OHTOMO, Toshiniko
APPLICANT: SATO, Koh
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: MEDULLOBLASTOMA CELLS
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646, 265A
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP94/01763
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-291078

FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/184
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-646-265A-47

Query Match
Best Local Similarity 90.5%; Score 506; DB 4; Length 126;
Best Local Similarity 90.7%; Pred. No. 2,4e-40;
Matches 97; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSLSASVDRTYITCKASQNGTNAVYQQRGKAPKALISASFLYSGVPY 60
|||||
DB 20 DIQMTQSPSLSASVDRTYITCKASQNGTNAVYQQRGKAPKALISASFLYSGVPS 79
|||||

QY 61 RFSGSSGTDFTLTISLQPEDPATYCCQYNYPLTFGGGTVEIK 107
|||||
DB 80 RFSGSSGTDFTLTISLQPEDPATYCCQYNYSPRAFGGTVEIK 126
|||||

RESULT 7
US-08-646-265A-51
Sequence 51, Application US/08646265A
Patent No. 6214973
GENERAL INFORMATION:
APPLICANT: OHTOMO, Toshiniko
APPLICANT: SATO, Koh
APPLICANT: TSUCHIYA, Masayuki
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,265A
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP94/01763
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-291078
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/184
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:

LENGTH: 126 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-646-265A-51

Query Match
Best Local Similarity 90.3%; Score 505; DB 4; Length 126;
Best Local Similarity 90.7%; Pred. No. 2,9e-40;
Matches 97; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSLSASVDRTYITCKASQNGTNAVYQQRGKAPKALISASFLYSGVPY 60
|||||
DB 20 DIQMTQSPSLSASVDRTYITCKASQNGTNAVYQQRGKAPKALISASFLYSGVPS 79
|||||

QY 61 RFSGSSGTDFTLTISLQPEDPATYCCQYNYPLTFGGGTVEIK 107
|||||
DB 80 RFSGSSGTDFTLTISLQPEDPATYCCQYNYSPRAFGGTVEIK 126
|||||

RESULT 8
US-08-646-265A-57
Sequence 57, Application US/08646265A
Patent No. 6214973
GENERAL INFORMATION:
APPLICANT: OHTOMO, Toshiniko
APPLICANT: SATO, Koh
APPLICANT: TSUCHIYA, Masayuki
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,265A
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP94/01763
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-291078
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/184
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-646-265A-57

Query Match
Best Local Similarity 90.2%; Score 504; DB 4; Length 126;
Best Local Similarity 89.7%; Pred. No. 3,6e-40;
Matches 96; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSLSASVDRTYITCKASQNGTNAVYQQRGKAPKALISASFLYSGVPY 60
|||||

```
Db 20 DIQMTQSPSSLSASVGDVNTTCRKASQNVGTNAVYQOKPGKAPKALITYSASFUSYGVPS 79
      |||
Qy 61 RFSGSGSTDFLTITSSIQPEDFATYYCOQYNIYPLTFGQGTKEIK 107
      |||
Db 80 RFSGSGSTDFLTITSSIQPEDFATYYCOQYNSYPRAFGQGTKEIK 126

RESULT 9
US-08-646-265A-63
; Sequence 63, Application US/08646265A
; Patent No. 6214973
; GENERAL INFORMATION:
; APPLICANT: OHTOMO, Toshiniko
; APPLICANT: SATO, Koh
; APPLICANT: TSUCHIYA, Masayuki
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: MEDULLOBLASTOMA CELLS
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,265A
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JP94/01763
; FILING DATE: 19-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-291078
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/184
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEFAX: 904136
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 126 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-646-265A-63

Query Match 90.2%; Score 504; DB 4; Length 126;
Best Local Similarity 89.7%; Pred. No. 3.6e-40;
Matches 96; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDVNTTCRKASQNVGTNAVYQOKPGKAPKALITYSASFUSYGVPS 60
      |||
Db 20 DIQMTQSPSSLSASVGDVNTTCRKASQNVGTNAVYQOKPGKAPKALITYSASFUSYGVPS 79

Qy 61 RFSGSGSTDFLTITSSIQPEDFATYYCOQYNIYPLTFGQGTKEIK 107
      |||
Db 80 RFSGSGSTDFLTITSSIQPEDFATYYCOQYNSYPRAFGQGTKEIK 126

RESULT 10
US-08-646-265A-131
; Sequence 131, Application US/08646265A

Patent No. 6214973
; GENERAL INFORMATION:
; APPLICANT: OHTOMO, Toshiniko
; APPLICANT: SATO, Koh
; APPLICANT: TSUCHIYA, Masayuki
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: MEDULLOBLASTOMA CELLS
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,265A
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JP94/01763
; FILING DATE: 19-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-291078
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/184
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEFAX: 904136
; INFORMATION FOR SEQ ID NO: 131:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-646-265A-131

Query Match 89.8%; Score 502; DB 4; Length 107;
Best Local Similarity 89.7%; Pred. No. 4.7e-40;
Matches 96; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDVNTTCRKASQNVGTNAVYQOKPGKAPKALITYSASFUSYGVPS 60
      |||
Db 1 DIQMTQSPSSLSASVGDVNTTCRKASQNVGTNAVYQOKPGKAPKALITYSASFUSYGVPS 60

Qy 61 RFSGSGSTDFLTITSSIQPEDFATYYCOQYNIYPLTFGQGTKEIK 107
      |||
Db 61 RFSGSGSTDFLTITSSIQPEDFATYYCOQYNSYPRAFGQGTKEIK 107

RESULT 11
US-08-646-265A-53
; Sequence 53, Application US/08646265A
; Patent No. 6214973
; GENERAL INFORMATION:
; APPLICANT: OHTOMO, Toshiniko
; APPLICANT: SATO, Koh
; APPLICANT: TSUCHIYA, Masayuki
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: MEDULLOBLASTOMA CELLS
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
```

```

: CITY: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20007-5109
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/646,265A
: FILING DATE: 09-SEP-1996
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: WO PCT/JP94/011763
: FILING DATE: 19-OCT-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 5-291078
: FILING DATE: 19-NOV-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: WEGNER, Harold C.
: REGISTRATION NUMBER: 25,258
: REFERENCE/DOCKET NUMBER: 53466/184
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202)672-5300
: TELEFAX: (202)672-5399
: TELEX: 904136
: INFORMATION FOR SEQ ID NO: 53:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 126 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-646-265A-53

Query Match      89.8%; Score 502; DB 4; Length 126;
Best Local Similarity 89.7%; Pred. No. 5.6e-40;
Matches 96; Conservative 3; Mismatches 8; Indels 0; Gaps 0:

QY 1 DIOMTQSPSSLSASVGDRTYITCKASQNGTNNVWYQKPKGAPKALISASFLYSGVPY 60
   |||||||
DB 20 DIOMTQSPSSLSASVGDRTYITCKASQNGTNNVWYQKPKGAPKALISASFLYSGVPS 79
   |||||||

QY 61 RRSQSGSGTDFLTITSSLOPEDFATYYCOQYNINYPITFGQGTKEIK 107
   |||||||
DB 80 RRSQSGSGTDFLTITSSLOPEDFATYYCOQYNINYPITFGQGTKEIK 126
   |||||||

RESULT 12
US-08-646-265A-85
: Sequence 85, Application US/08646265A
: Patent No. 6214973
: GENERAL INFORMATION:
: APPLICANT: OHTOMO, Toshihiko
: APPLICANT: SATO, Koh
: APPLICANT: TSUCHIYA, Masayuki
: TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
: NUMBER OF SEQUENCES: 132
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Foley & Lardner
: STREET: 3000 K Street, N.W., Suite 500
: CITY: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20007-5109
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/646,265A
```

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: FILING DATE: 09-SEP-1996
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: WO PCT/JP94/011763
: FILING DATE: 19-OCT-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 5-291078
: FILING DATE: 19-NOV-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: WEGNER, Harold C.
: REGISTRATION NUMBER: 25,258
: REFERENCE/DOCKET NUMBER: 53466/184
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202)672-5300
: TELEFAX: (202)672-5399
: TELEX: 904136
: INFORMATION FOR SEQ ID NO: 85:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 126 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-646-265A-85

Query Match      89.8%; Score 502; DB 4; Length 126;
Best Local Similarity 89.7%; Pred. No. 5.6e-40;
Matches 96; Conservative 3; Mismatches 8; Indels 0; Gaps 0:

QY 1 DIOMTQSPSSLSASVGDRTYITCKASQNGTNNVWYQKPKGAPKALISASFLYSGVPY 60
   |||||||
DB 20 DIOMTQSPSSLSASVGDRTYITCKASQNGTNNVWYQKPKGAPKALISASFLYSGVPS 79
   |||||||

QY 61 RRSQSGSGTDFLTITSSLOPEDFATYYCOQYNINYPITFGQGTKEIK 107
   |||||||
DB 80 RRSQSGSGTDFLTITSSLOPEDFATYYCOQYNINYPITFGQGTKEIK 126
   |||||||

RESULT 13
US-08-646-265A-87
: Sequence 87, Application US/08646265A
: Patent No. 6214973
: GENERAL INFORMATION:
: APPLICANT: OHTOMO, Toshihiko
: APPLICANT: SATO, Koh
: APPLICANT: TSUCHIYA, Masayuki
: TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
: NUMBER OF SEQUENCES: 132
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Foley & Lardner
: STREET: 3000 K Street, N.W., Suite 500
: CITY: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20007-5109
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/646,265A
: FILING DATE: 09-SEP-1996
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: WO PCT/JP94/011763
: FILING DATE: 19-OCT-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 5-291078
: FILING DATE: 19-NOV-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: WEGNER, Harold C.
: REGISTRATION NUMBER: 25,258
```


REFERENCE/DOCKET NUMBER: 53466/184
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-646-265A-87

Query Match
Best Local Similarity 89.7%; Score 502; DB 4; Length 126;
Matches 96; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIOMTQSPSSLSASVGDVDTITCKASQNVGTNAVYQOKPGKAPKALITYSASFLYSGVPY 60
|||||
DB 20 DIOMTQSPSSLSASVGDVDTITCKASQNVGTNAVYQOKPGKAPKALITYSASFLYSGVPS 79
|||||

QY 61 RFSGSGSGTDFTLTITSSLOPEDFATYYCOQYNIYPLTFGGGTKEIK 107
|||||

DB 80 RFSGSGSGTDFTLTITSSLOPEDFATYYCOQYNIYPLTFGGGTKEIK 126
|||||

RESULT 14
US-08-646-265A-59
Sequence 59, Application US/08646265A
Patent No. 6214973
GENERAL INFORMATION:
APPLICANT: OHTOMO, Toshiniko
APPLICANT: SATO, Koh
APPLICANT: TSUCHIYA, Masayuki
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
NUMBER OF SEQUENCES: 132
TITLE OF INVENTION: MEDULLOBLASTOMA CELLS
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,265A
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP94/01763
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-291078
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/184
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-646-265A-59

Query Match
Best Local Similarity 89.4%; Score 500; DB 4; Length 126;
Matches 95; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIOMTQSPSSLSASVGDVDTITCKASQNVGTNAVYQOKPGKAPKALITYSASFLYSGVPY 60
|||||
DB 20 DIOMTQSPSSLSASVGDVDTITCKASQNVGTNAVYQOKPGKAPKALITYSASFLYSGVPS 79
|||||

QY 61 RFSGSGSGTDFTLTITSSLOPEDFATYYCOQYNIYPLTFGGGTKEIK 107
|||||

DB 80 RFSGSGSGTDFTLTITSSLOPEDFATYYCOQYNIYPLTFGGGTKEIK 126
|||||

RESULT 15
US-08-646-265A-75
Sequence 75, Application US/08646265A
Patent No. 6214973
GENERAL INFORMATION:
APPLICANT: OHTOMO, Toshiniko
APPLICANT: SATO, Koh
APPLICANT: TSUCHIYA, Masayuki
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
NUMBER OF SEQUENCES: 132
TITLE OF INVENTION: MEDULLOBLASTOMA CELLS
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,265A
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP94/01763
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-291078
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/184
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-646-265A-75

Query Match
Best Local Similarity 88.8%; Score 498; DB 4; Length 126;
Matches 95; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIOMTQSPSSLSASVGDVDTITCKASQNVGTNAVYQOKPGKAPKALITYSASFLYSGVPY 60
|||||
DB 20 DIOMTQSPSSLSASVGDVDTITCKASQNVGTNAVYQOKPGKAPKALITYSASFLYSGVPS 79
|||||

QY 61 RFSGSGSGTDFTLTITSSLOPEDFATYYCOQYNIYPLTFGGGTKEIK 107
|||||

Db 80 RPSGSGSTDFTLTSSLOPEDIDYFCQQYNSYPRAFGQTKVEIK 126

Search completed: April 2, 2003, 14:40:36
Job time : 29 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 2, 2003, 14:39:14 ; Search time 34 Seconds
(without alignments)
192.399 Million cell updates/sec

Title: US-09-875-221B-9

Perfect score: 559
Sequence: 1 DIOMTOSPSLSASVGDRTV.....COQYNYPLFRGQGTKEIK 107

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 248812 seqs, 61136040 residues

Total number of hits satisfying chosen parameters: 248812

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

1: /cgn2_6/ptodata/2/pubpaa/US08_NEM_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCR_NEM_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEM_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEM_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/PCUTS_PUBCOMB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09_NEM_PUB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US10_NEM_PUB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEM_PUB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	559	100.0	107	9	US-09-875-221A-9
2	559	100.0	107	9	US-09-949-559-9
3	559	100.0	214	9	US-09-875-221A-128
4	559	100.0	214	10	US-09-949-559-128
5	554	99.1	107	9	US-09-875-221A-11
6	554	99.1	107	10	US-09-949-559-11
7	520	93.0	107	10	US-09-905-243-77
8	513	91.8	126	9	US-09-749-873-65
9	509	91.1	107	9	US-09-749-873-130
10	509	91.1	126	9	US-09-749-873-43
11	509	91.1	126	9	US-09-749-873-91
12	509	91.1	269	9	US-09-749-873-109
13	506	90.5	126	9	US-09-749-873-47
14	505	90.3	126	9	US-09-749-873-51
15	504	90.2	126	9	US-09-749-873-57
16	504	90.2	126	9	US-09-749-873-63
17	502	89.8	107	9	US-09-749-873-131
18	502	89.8	126	9	US-09-749-873-53
19	502	89.8	126	9	US-09-749-873-85

20	502	89.8	126	9	US-09-749-873-87	Sequence 87, Appl
21	500	89.4	126	9	US-09-749-873-59	Sequence 59, Appl
22	498	89.1	126	9	US-09-749-873-75	Sequence 75, Appl
23	497	88.9	102	10	US-09-905-243-80	Sequence 80, Appl
24	497	88.9	109	10	US-09-811-123-5	Sequence 5, Appl
25	497	88.9	126	9	US-09-749-873-69	Sequence 69, Appl
26	497	88.9	126	9	US-09-749-873-77	Sequence 77, Appl
27	491	87.8	126	9	US-09-749-873-73	Sequence 73, Appl
28	484	86.6	126	9	US-09-749-873-81	Sequence 81, Appl
29	481	86.0	108	10	US-09-971-543-7	Sequence 7, Appl
30	481	86.0	252	10	US-09-971-543-1	Sequence 1, Appl
31	474	84.8	108	10	US-09-056-160B-12	Sequence 12, Appl
32	474	84.8	109	10	US-09-811-123-6	Sequence 6, Appl
33	472	84.4	108	9	US-09-875-221A-104	Sequence 104, App
34	472	84.4	108	9	US-09-949-559-104	Sequence 104, App
35	469	83.9	107	9	US-10-035-637-2	Sequence 2, Appl
36	466	83.4	126	9	US-09-269-921-106	Sequence 106, App
37	466	83.4	126	10	US-09-760-723-6	Sequence 6, Appl
38	466	83.4	126	10	US-09-355-925-6	Sequence 6, Appl
39	464.5	83.1	109	9	US-09-726-258-47	Sequence 47, Appl
40	464	83.0	105	10	US-09-974-449-4	Sequence 4, Appl
41	464	83.0	211	10	US-09-974-449-36	Sequence 36, Appl
42	463	82.8	108	9	US-09-910-483-3	Sequence 3, Appl
43	463	82.8	108	9	US-09-910-483-7	Sequence 7, Appl
44	463	82.8	108	9	US-09-910-483-11	Sequence 11, Appl
45	463	82.8	108	9	US-09-910-483-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1

US-09-875-221A-9
; Sequence 9, Application US/09875221A
; Publication No. US20030026805A1
; GENERAL INFORMATION:
; APPLICANT: Athwal, Diljeet Singh
; APPLICANT: Brown, Derek Thomas
; APPLICANT: Weir, Andrew Neil Charles
; APPLICANT: Popplewell, Andrew George
; APPLICANT: Chapman, Andrew Paul
; APPLICANT: King, David John
; TITLE OF INVENTION: Biological Products
; FILE REFERENCE: Carp-0089
; CURRENT APPLICATION NUMBER: US/09/875,221A
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: GB0013810.7
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: htf40-gli
US-09-875-221A-9

Query Match 100.0%; Score 559; DB 9; Length 107;
Best local similarity 100.0%; Pred. No. 5e-34;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIOMTOSPSLSASVGDRTTICKASQNVGTWVANYQOKRGAAPALISAFSLYSGVPY 60
|||||
DB 1 DIOMTOSPSLSASVGDRTTICKASQNVGTWVANYQOKRGAAPALISAFSLYSGVPY 60
|||||
QY 61 RSSGSGSGTDFLTITSSLOPEDFATYYCOQYNYPLFRGQGTKEIK 107
|||||
DB 61 RSSGSGSGTDFLTITSSLOPEDFATYYCOQYNYPLFRGQGTKEIK 107
|||||

RESULT 2
US-09-949-559-9

Sequence 9, Application US/09949559
Patent No. US20020151682A1
GENERAL INFORMATION:
APPLICANT: Athwal, Diljeet Singh
APPLICANT: Brown, Derek Thomas
APPLICANT: Weir, Andrew Neil Charles
APPLICANT: Popplewell, Andrew George
APPLICANT: Chapman, Andrew Paul
APPLICANT: King, David John
TITLE OF INVENTION: Biological Products
FILE REFERENCE: Carp-0095
CURRENT APPLICATION NUMBER: US/09/949,559
CURRENT FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: 0013810.7GB
PRIOR FILING DATE: 2000-06-06
PRIOR APPLICATION NUMBER: 09/875,221
PRIOR FILING DATE: 2001-06-06
NUMBER OF SEQ ID NOS: 130
SOFTWARE: PatentIn version 3.1
SEQ ID NO 9
LENGTH: 107
TYPE: PRF
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: hTF40-gL1
US-09-949-559-9

Query Match 100.0%; Score 559; DB 10; Length 107;
Best Local Similarity 100.0%; Pred. No. 5e-34;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIOMTOSPSLSASVGDRTYITCKASONGTNAVYQOKRGPAPKALISASFLYSGVPY 60
DB 1 DIOMTOSPSLSASVGDRTYITCKASONGTNAVYQOKRGPAPKALISASFLYSGVPY 60
QY 61 RFSGSGSGTDFLTITSSLOPEDFATYCCOYNIYPLTFGGGTVEIK 107
DB 61 RFSGSGSGTDFLTITSSLOPEDFATYCCOYNIYPLTFGGGTVEIK 107

RESULT 3
US-09-875-221A-128
Sequence 128, Application US/09875221A
Publication No. US20030026805A1
GENERAL INFORMATION:
APPLICANT: Athwal, Diljeet Singh
APPLICANT: Brown, Derek Thomas
APPLICANT: Weir, Andrew Neil Charles
APPLICANT: Popplewell, Andrew George
APPLICANT: Chapman, Andrew Paul
APPLICANT: King, David John
TITLE OF INVENTION: Biological Products
FILE REFERENCE: Carp-0089
CURRENT APPLICATION NUMBER: US/09/875,221A
CURRENT FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: GB0013810.7
PRIOR FILING DATE: 2000-06-06
NUMBER OF SEQ ID NOS: 130
SOFTWARE: PatentIn version 3.1
SEQ ID NO 128
LENGTH: 214
TYPE: PRF
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Grafted light chain for fab and modified fab
US-09-875-221A-128

Query Match 100.0%; Score 559; DB 9; Length 214;
Best Local Similarity 100.0%; Pred. No. 8.8e-34;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIOMTOSPSLSASVGDRTYITCKASONGTNAVYQOKRGPAPKALISASFLYSGVPY 60
DB 1 DIOMTOSPSLSASVGDRTYITCKASONGTNAVYQOKRGPAPKALISASFLYSGVPY 60

DB 1 DIOMTOSPSLSASVGDRTYITCKASONGTNAVYQOKRGPAPKALISASFLYSGVPY 60
QY 61 RFSGSGSGTDFLTITSSLOPEDFATYCCOYNIYPLTFGGGTVEIK 107
DB 61 RFSGSGSGTDFLTITSSLOPEDFATYCCOYNIYPLTFGGGTVEIK 107

RESULT 4
US-09-949-559-128
Sequence 128, Application US/09949559
Patent No. US20020151682A1
GENERAL INFORMATION:
APPLICANT: Athwal, Diljeet Singh
APPLICANT: Brown, Derek Thomas
APPLICANT: Weir, Andrew Neil Charles
APPLICANT: Popplewell, Andrew George
APPLICANT: Chapman, Andrew Paul
APPLICANT: King, David John
TITLE OF INVENTION: Biological Products
FILE REFERENCE: Carp-0095
CURRENT APPLICATION NUMBER: US/09/949,559
CURRENT FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: 0013810.7GB
PRIOR FILING DATE: 2000-06-06
PRIOR APPLICATION NUMBER: 09/875,221
PRIOR FILING DATE: 2001-06-06
NUMBER OF SEQ ID NOS: 130
SOFTWARE: PatentIn version 3.1
SEQ ID NO 128
LENGTH: 214
TYPE: PRF
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Grafted light chain for fab and modified fab
US-09-949-559-128

Query Match 100.0%; Score 559; DB 10; Length 214;
Best Local Similarity 100.0%; Pred. No. 8.8e-34;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIOMTOSPSLSASVGDRTYITCKASONGTNAVYQOKRGPAPKALISASFLYSGVPY 60
DB 1 DIOMTOSPSLSASVGDRTYITCKASONGTNAVYQOKRGPAPKALISASFLYSGVPY 60
QY 61 RFSGSGSGTDFLTITSSLOPEDFATYCCOYNIYPLTFGGGTVEIK 107
DB 61 RFSGSGSGTDFLTITSSLOPEDFATYCCOYNIYPLTFGGGTVEIK 107

RESULT 5
US-09-875-221A-11
Sequence 11, Application US/09875221A
Publication No. US20030026805A1
GENERAL INFORMATION:
APPLICANT: Athwal, Diljeet Singh
APPLICANT: Brown, Derek Thomas
APPLICANT: Weir, Andrew Neil Charles
APPLICANT: Popplewell, Andrew George
APPLICANT: Chapman, Andrew Paul
APPLICANT: King, David John
TITLE OF INVENTION: Biological Products
FILE REFERENCE: Carp-0089
CURRENT APPLICATION NUMBER: US/09/875,221A
CURRENT FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: GB0013810.7
PRIOR FILING DATE: 2000-06-06
NUMBER OF SEQ ID NOS: 130
SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
LENGTH: 107
TYPE: PRF
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: hnf40-gL2
US-09-875-221a-11

Query Match 99.1%; Score 554; DB 9; Length 107;
Best Local Similarity 99.1%; Pred. No. 1.1e-33;
Matches 106; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIOMTQSPSSLSASVGDRTVITCKASQNVGTNVAWYQKPKAKALITYSASFYSGVPY 60
DB 1 DIOMTQSPSSLSASVGDRTVITCKASQNVGTNVAWYQKPKAKALITYSASFYSGVPY 60
QY 61 RFGSGSGGTDFTLTISLSLOPEDFATYCCQYNYIPLTFGGGTKEIK 107
DB 61 RFGSGSGGTDFTLTISLSLOPEDFATYCCQYNYIPLTFGGGTKEIK 107

RESULT 6
US-09-949-559-11

Sequence 11, Application US/09949559
Patent No. US20020151682A1

GENERAL INFORMATION:

APPLICANT: Athwal, Diljeet Singh
APPLICANT: Brown, Derek Thomas
APPLICANT: Weir, Andrew Neil Charles
APPLICANT: Popplewell, Andrew George
APPLICANT: Chapman, Andrew Paul

TITLE OF INVENTION: Biological Products

FILE REFERENCE: Carp-0095

CURRENT APPLICATION NUMBER: US/09/949,559

CURRENT FILING DATE: 2001-12-20

PRIOR APPLICATION NUMBER: 0013810.7GB

PRIOR FILING DATE: 2000-06-06

PRIOR APPLICATION NUMBER: 09/875,221

PRIOR FILING DATE: 2001-06-06

NUMBER OF SEQ ID NOS: 130

SOFTWARE: Patentin version 3.1

SEQ ID NO 11

LENGTH: 107

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: hnf40-gL2

US-09-949-559-11

Query Match 99.1%; Score 554; DB 10; Length 107;
Best Local Similarity 99.1%; Pred. No. 1.1e-33;
Matches 106; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIOMTQSPSSLSASVGDRTVITCKASQNVGTNVAWYQKPKAKALITYSASFYSGVPY 60
DB 1 DIOMTQSPSSLSASVGDRTVITCKASQNVGTNVAWYQKPKAKALITYSASFYSGVPY 60
QY 61 RFGSGSGGTDFTLTISLSLOPEDFATYCCQYNYIPLTFGGGTKEIK 107
DB 61 RFGSGSGGTDFTLTISLSLOPEDFATYCCQYNYIPLTFGGGTKEIK 107

RESULT 7
US-09-905-243-77

Sequence 77, Application US/09905243
Patent No. US20020062009A1

GENERAL INFORMATION:

APPLICANT: Taylor, Alexander H

TITLE OF INVENTION: Monoclonal Antibodies with Reduced

FILE REFERENCE: P50770

CURRENT APPLICATION NUMBER: US/09/905,243

CURRENT FILING DATE: 2001-07-16

PRIOR APPLICATION NUMBER: 09/300,970

PRIOR FILING DATE: 1999-04-28

NUMBER OF SEQ ID NOS: 97

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 77
LENGTH: 107

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: murine/chimpanzee sequence

US-09-905-243-77

Query Match 93.0%; Score 520; DB 10; Length 107;
Best Local Similarity 94.4%; Pred. No. 3.2e-31;
Matches 101; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIOMTQSPSSLSASVGDRTVITCKASQNVGTNVAWYQKPKAKALITYSASFYSGVPY 60
DB 1 DIOMTQSPSSLSASVGDRTVITCKASQNVGTNVAWYQKPKAKALITYSASFYSGVPY 60
QY 61 RFGSGSGGTDFTLTISLSLOPEDFATYCCQYNSYPLTFGGGTKEIK 107
DB 61 RFGSGSGGTDFTLTISLSLOPEDFATYCCQYNSYPLTFGGGTKEIK 107

RESULT 8
US-09-749-873-65

Sequence 65, Application US/09749873
Publication No. US20030023045A1

GENERAL INFORMATION:

APPLICANT: OHTOMO, Toshiniko

SATO, Koh

TSUCHIYA, Masayuki

TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN

MEDULLOBLASTOMA CELLS

NUMBER OF SEQUENCES: 132

CORRESPONDENCE ADDRESS:

ADDRESSER: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/749,873

FILING DATE: 29-Dec-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/646,265

FILING DATE: 1996-09-09

APPLICATION NUMBER: JP 5-291078

FILING DATE: 19-NOV-1993

ATTORNEY/AGENT INFORMATION:

NAME: WEGNER, Harold C.

REGISTRATION NUMBER: 25,258

REFERENCE/DOCKET NUMBER: 53466/184

TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399

INFORMATION FOR SEQ ID NO: 65:

SEQUENCE CHARACTERISTICS:

LENGTH: 126 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 65:

Query Match 91.8%; Score 513; DB 9; Length 126;
Best Local Similarity 92.5%; Pred. No. 1.2e-30;
Matches 99; Conservative 1; Mismatches 7; Indels 0; Gaps 0;


```

ADDRESS: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/749,873
FILING DATE: 29-Dec-2000
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/646,265
FILING DATE: 1996-09-09
APPLICATION NUMBER: JP 5-291078
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/184
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 91:
US-09-749-873-91

Query Match          91.1%; Score 509; DB 9; Length 126;
Best Local Similarity 91.6%; Pred. No. 2.3e-30;
Matches 98; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTITCKASQNGTVNAMYQOKPGKAPKALISASFLYSGVPY 60
DB 20 DIQMTQSPSSLSASVGDRTITCKASQNGTVNAMYQOKPGKAPKALISASFLYSGVPS 79
QY 61 RFSSGSGTDFLTITSSLPEDFATYYCOQYNIYPLTFGQTKVEIK 107
DB 80 RFSSGSGTDFLTITSSLPEDFATYYCOQYNSYPRAFQGTKEIK 126

RESULT 12
US-09-749-873-109
Sequence 109, Application US/09/749873
Publication No. US20030023045A1
GENERAL INFORMATION:
APPLICANT: OHTOMO, Toshihiko
SATO, Koh
TSUCHIYA, Masayuki
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
MEDULLOBLASTOMA CELLS
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30

```

```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/749,873
FILING DATE: 29-Dec-2000
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/646,265
FILING DATE: 1996-09-09
APPLICATION NUMBER: JP 5-291078
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/184
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 109:
SEQUENCE CHARACTERISTICS:
LENGTH: 269 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 109:
US-09-749-873-109

Query Match          91.1%; Score 509; DB 9; Length 269;
Best Local Similarity 91.6%; Pred. No. 4.2e-30;
Matches 98; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTITCKASQNGTVNAMYQOKPGKAPKALISASFLYSGVPY 60
DB 155 DIQMTQSPSSLSASVGDRTITCKASQNGTVNAMYQOKPGKAPKALISASFLYSGVPS 214
QY 61 RFSSGSGTDFLTITSSLPEDFATYYCOQYNIYPLTFGQTKVEIK 107
DB 215 RFSSGSGTDFLTITSSLPEDFATYYCOQYNSYPRAFQGTKEIK 261

RESULT 13
US-09-749-873-47
Sequence 47, Application US/09/749873
Publication No. US20030023045A1
GENERAL INFORMATION:
APPLICANT: OHTOMO, Toshihiko
SATO, Koh
TSUCHIYA, Masayuki
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
MEDULLOBLASTOMA CELLS
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/749,873
FILING DATE: 29-Dec-2000
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/646,265
FILING DATE: 1996-09-09
APPLICATION NUMBER: JP 5-291078
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.

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1      REGISTRATION NUMBER: 25, 258
2      REFERENCE/DOCKET NUMBER: 53466/184
3      TELECOMMUNICATION INFORMATION:
4      TELEPHONE: (202)672-5300
5      TELEFAX: (202)672-5399
6      TELEX: 904136
7      INFORMATION FOR SEQ ID NO: 47:
8      SEQUENCE CHARACTERISTICS:
9          LENGTH: 126 amino acids
10         TYPE: amino acid
11         TOPOLOGY: linear
12     MOLECULE TYPE: protein
13     SEQUENCE DESCRIPTION: SEQ ID NO: 47:
14     US-09-749-873-47
15
16 Query Match           90.5%: Score 506; DB 9; Length 126;
17 Best Local Similarity 90.7%; Pred. No. 3,7e-30;
18 Matches   97: Conservative    2; Mismatches    8; Indels    0; Gaps    0;
19
20 QY       1 DIQMTPSSSLASVAGDRTITCKASQNGTVWAVYQKPGKAPRALIYSASFILSYGVPY 60
21             |||||
22 Db        20 DIQMTPSSSLASVAGDRTITCKASQNGTVWAVYQKPGKAPRLIIYSASYRSGVPS 79
23             |||||
24 QY       61 RRSGGSGTDFLLTISSLQPEDPFIATYYCCQNYIITPLTGQGTRVEIK 107
25             |||||
26 Db        80 RRSGGSGTDYFTLTISLQPEDIAFYTCQNYNSPRAFQGTGRVEIK 126
27             |||||
28 RESULT 14
29 US-09-749-873-51
30 : Sequence 51, Application US/09749873
31 : Publication NO. US20030023045A1
32 : GENERAL INFORMATION:
33     APPLICANT: OHTOMO, Toshihiko
34     SATO, Koh
35     TSUCHIYA, Masayuki
36     TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
37                     MEDULLOBLASTOMA CELLS
38     NUMBER OF SEQUENCES: 132
39     CORRESPONDENCE ADDRESS:
40         ADDRESSEE: Foley & Lardner
41         STREET: 3000 K Street, N.W., Suite 500
42         CITY: Washington
43         STATE: D.C.
44         COUNTRY: USA
45         ZIP: 20007-5109
46     COMPUTER READABLE FORM:
47         MEDIUM TYPE: floppy disk
48         COMPUTER: IBM PC compatible
49         OPERATING SYSTEM: PC-DOS/MS-DOS
50         SOFTWARE: PatentIn Release #1.0, Version #1.30
51     CURRENT APPLICATION DATA:
52         APPLICATION NUMBER: US/09/749,873
53         FILING DATE: 29-Dec-2000
54         CLASSIFICATION: <Unknown>
55     PRIOR APPLICATION DATA:
56         APPLICATION NUMBER: 08/646,265
57         FILING DATE: 1996-09-09
58         APPLICATION NUMBER: JP 5-291078
59         FILING DATE: 19-NOV-1993
60     ATTORNEY/AGENT INFORMATION:
61         NAME: WEGNER, Harold C.
62         REGISTRATION NUMBER: 25, 258
63         REFERENCE/DOCKET NUMBER: 53466/184
64     TELECOMMUNICATION INFORMATION:
65         TELEPHONE: (202)672-5300
66         TELEFAX: (202)672-5399
67         TELEX: 904136
68     INFORMATION FOR SEQ ID NO: 51:
69     SEQUENCE CHARACTERISTICS:
70         LENGTH: 126 amino acids
71         TYPE: amino acid
72         TOPOLOGY: linear

```

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: MOLECULE TYPE: protein
: SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-09-749-873-51

Query Match          90.3%, Score 505; DB 9; Length 126;
Best Local Similarity 90.7%; Pred. No. 4,4e-30;
Matches 97; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

OY 1 DIOMQSPSSLSASVGDVVTITCKRSONVGNVANYOOKPGKAPKALITYSASFITYSGVPY 60
DB 20 DIOMQSPSSLSASVGDRTTITCKRSONVGNVANYOQKPGKAPKALITYSASIRISGVPS 79
QY 61 RFSGSGGTDFLTITISLQPEDFATYYCOQYNIYLFEGQGTKEIK 107
DB 80 RFSGSGGTDFLTITISLQPEDIATYFCQYNSYPRAFQGTKEIK 126

RESULT 15
US-09-749-873-57
: Sequence 57, Application US/09749873
: Publication No. US20030023045A1
GENERAL INFORMATION:
APPLICANT: OHTOMO, Toshihiko
SATO, Koh
TSUCHIYA, Masayuki
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
MEDULLOBLASTOMA CELLS
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/749, 873
FILING DATE: 29-Dec-2000
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/646,265
FILING DATE: 1996-09-09
APPLICATION NUMBER: JP 5-291078
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/184
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 57:
US-09-749-873-57

Query Match          90.2%, Score 504; DB 9; Length 126;
Best Local Similarity 89.7%; Pred. No. 5.2e-30;
Matches 96; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

OY 1 DIOMQSPSSLSASVGDVVTITCKRSONVGNVANYOOKPGKAPKALITYSASFITYSGVPY 60
DB 20 DIOMQSPSSLSASVGDVVTITCKRSONVGNVANYOQKPGKAPKALITYSASIRISGVPS 79

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Thu Apr 3 08:53:30 2003

us-09-875-221b-9.rapb

Page 7

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61 RFGSGGGTDTLTITSLQPEDFATYYCQYNIPLTFGGQTKVEIK 107
      |||||
80 RFSSGGSGTDTFTTISLQPEDATATYYCQYNSVPRAFGQGTKEIK 126

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Search completed: April 2, 2003, 14:48:11
Job time : 35 secs

This Page Blank (uspto)

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 2, 2003, 14:35:09 ; Search time 43 Seconds
(without alignments)
239.218 Million cell updates/sec

Title: US-09-875-221b-9

Perfect score: 559

Sequence: 1 DIQMTQSPSSLSASVGDRTV.....CQGYNYPLTFGQGTKEIK 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	470	84.1	125	2 S40333	Ig kappa chain V-J
2	468	83.7	125	2 S40349	Ig kappa chain V-J
3	467	83.5	107	2 I69017	anti-HIV envelope
4	466	83.4	129	2 S40369	Ig kappa chain - h
5	462	82.6	108	1 K1HUBN	Ig kappa chain V-I
6	462	82.6	123	2 S40313	Ig kappa chain V-J
7	459	82.1	125	2 S40353	Ig kappa chain V-J
8	457	81.8	117	2 S46371	Ig kappa chain V-J
9	454	81.2	107	2 S36264	Ig kappa chain V
10	452	80.9	123	2 S40331	Ig kappa chain - h
11	451	80.7	108	2 B49047	Ig kappa chain V-I
12	450	80.5	108	1 K1HUBU	Ig kappa chain V-I
13	450	80.5	117	2 S46376	Ig kappa chain V-J
14	450	80.5	131	2 S40352	Ig kappa chain V-J
15	450	80.5	132	2 S40334	Ig kappa chain - h
16	448.5	80.2	124	2 S40336	Ig kappa chain V-J
17	448	80.1	108	2 S36279	Ig kappa chain V
18	447	80.0	107	2 S36277	Ig kappa chain V
19	446	79.8	107	2 S36269	Ig kappa chain V
20	446	79.8	108	1 K1HUGL	Ig kappa chain V-I
21	446	79.8	127	2 S40367	Ig kappa chain V-J
22	445	79.6	129	2 S40317	Ig kappa chain V-I
23	444	79.4	128	2 S46372	Ig kappa chain - h
24	444	79.2	108	2 S19674	Ig kappa chain V-I
25	443	79.2	129	2 S52793	Ig kappa chain V-I
26	443	79.2	108	1 K1HOLY	Ig kappa chain V-I
27	442	78.8	107	2 S36275	Ig kappa chain V
28	440.5	78.7	108	1 K1HUCU	Ig kappa chain V-I
29	440	78.7	108	1 K1HUCU	Ig kappa chain V-I

30	439.5	78.6	107	1 K1HUR	Ig kappa chain V-I
31	439	78.5	132	2 S38646	Ig kappa chain V-I
32	438	78.4	129	2 S52789	Ig kappa chain V-I
33	437	78.2	107	2 S36262	Ig kappa chain V
34	437	78.2	124	2 S40318	Ig kappa chain V-I
35	435	77.8	125	2 S40350	Ig kappa chain - h
36	435	77.8	125	2 S40350	Ig kappa chain - h
37	435	77.8	127	2 S11240	Ig kappa chain V-I
38	434	77.6	108	1 K1HUBU	Ig kappa chain V-I
39	434	77.6	126	2 S40335	Ig kappa chain V-I
40	434	77.6	130	2 S40368	Ig kappa chain V-I
41	433.5	77.5	107	2 S47183	Ig kappa chain - h
42	433	77.5	108	2 S44122	Ig kappa chain V-I
43	433	77.5	122	2 S40370	Ig kappa chain V-I
44	432.5	77.4	108	2 S30521	Ig kappa chain V-I
45	432	77.3	108	1 K1HURU	Ig kappa chain V-I

ALIGNMENTS

RESULT 1

Ig kappa chain V-J region - human

C:Species: Homo sapiens (man)

C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C:Accession: S40333

R:Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A:Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40333

A>Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-125 <RLE>

A:Cross-references: EMBL:X72443; NID:9441354; PIDN:CAA5111.1; PID:9441355

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-108/Domain: immunoglobulin homology <IMM>

Query Match 84.1%; Score 470; DB 2; Length 125;

Best Local Similarly 84.1%; Pred. No. 1e-33;

Matches 90; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCKASQNVGNVAMYOOKPEKARALYTSASFYSGVPY 60

DB 19 DIQMTQSPSSLSASVGDRTVITCKASQISWLMAYOOPKARALYTSASFYSGVPS 78

QY 61 RFSGSGSGTDEFTLTISSLQPEDFATVYCCQYNYPLTFGQGTKEIK 107

DB 79 RFSGSGSGTDEFTLTISSLQPEDFATVYCCQYNSYPMWTFGQGTKEIK 125

RESULT 2

Ig kappa chain V-J region - human

C:Species: Homo sapiens (man)

C:Date: 19-May-1994 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000

C:Accession: S40349

R:Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A:Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40349

A>Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-125 <RLE>

A:Cross-references: EMBL:X72459; NID:9441386; PIDN:CAA51127.1; PID:9441387

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:35-107/Domain: immunoglobulin homology <IMM>

Query Match 83.7%; Score 468; DB 2; Length 125;

```

QY      2  IQMTPSSSLASVGDRTYITTCASQNGTNVAMVYQOKPKAPKALYTSASFLYSGVPR 61
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      19  IQLTPSSSLASVADRTYITTCRASQGISALAWYQOKPKAPKLLIYDASSLESGVPSR 78
QY      62  FSGSGGTFDTLTISLQPEDFATYTCQQYNYITPLTFGSGTKVEIK 107
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      79  FSGSGGTFDTLTISLQPEDFATYTCQQYNYITPLTFGSGTKVEIK 124

RESULT 3
169017
anti-HIV1 envelope protein gp120 V3 loop monoclonal antibody L chain V region - human (4
C:Species: Homo sapiens (man)
C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jan-2000
C:Accession: 169017
R:Chn, L:n, Dueñas, M.; Levi, M.; Hinkula, J.; Mahren, B.; Borrebaeck, C.A.
Immunol. Lett. 44, 25-30, 1995
A:Title: Molecular characterization of a human anti-HIV 1 monoclonal antibody revealed a
A:Reference number: 154563; MUID:95237884; PMID:7721339
A:Accession: 169017
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: mRNA
A:Residues: 1-107 <RCS>
A:Cross-references: GB:S77140; NID:9913352; PIDN:AAB34102.1; PID:9913353
C:Genetics:
A:Gene: Ig Vkappa
C:Superfamily: Immunoglobulin V region: immunoglobulin homology
F:16-90/Domain: immunoglobulin homology <IM>

Query Match      83.5%; Score 467; DB 2; Length 107;
Best Local Similarity 83.2%; Pred. No. 1.6e-33;
Matches 89; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

QY      1  DIQMTPSSSLASVGDRTYITTCASQNGTNVAMVYQOKPKAPKALYTSASFLYSGVPR 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      1  DIQYTPSSSLASVGDRTYITTCRASHDIGSTLAWYQOKPEKAPSLIYASSLSQSGVPS 60
QY      61  FSGSGGTFDTLTISLQPEDFATYTCQQYNYITPLTFGSGTKVEIK 107
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      61  FSGSGGTFDTLTISLQPEDFATYTCQQYNSVITFGGSGTKVLIK 107

RESULT 4
S40369
Ig kappa chain - human
C:Species: Homo sapiens (man)
C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40369
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chl genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40369
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-129 <KIE>
A:Cross-references: EMBL:X72479; NID:9441426; PIDN:CAA51147.1; PID:9441427
C:Superfamily: Immunoglobulin V region: immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:37-111/Domain: immunoglobulin homology <IM>

Query Match      83.4%; Score 466; DB 2; Length 129;
Best Local Similarity 82.2%; Pred. No. 2.3e-33;
Matches 88; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

QY      1  DIQMTPSSSLASVGDRTYITTCASQNGTNVAMVYQOKPKAPKALYTSASFLYSGVPR 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      22  DIQMTPSSSLASVADRTYITTCRASHVISHNLVWFQOKPKAPKRSLLIYASSLSQSGVPS 81
QY      61  FSGSGGTFDTLTISLQPEDFATYTCQQYNYITPLTFGSGTKVEIK 107

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[illegible]

```
Dh 17 DIOMTQSPSSLSASVGDVVTTCRASQGIKNDLAWFOQKPKAKRLIYDAASLISGVPS 76
Oy 61 RFSGSGSGTDFLTITSSLOPEDFATYTCQOQYNIPLTFGOGTKVEIK 107
Db 77 RFSGSGSGTDFLTITSSLOPEDFATYTCQOQYNIPLTFGOGTKVEIK 123

RESULT 7
S40353
Ig kappa chain V-J-C region - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40353
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40353
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-125 <KLE>
A:Cross-references: EMBL:X72463
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:30-104/Domain: immunoglobulin homology <IMM>

Query Match 82.1%; Score 459; DB 2; Length 125;
Best Local Similarity 81.3%; Pred. No. 9.1e-33;
Matches 87; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

Oy 1 DIOMTQSPSSLSASVGDVVTTCRASQNVGTNVMYQOKPKAKRLIYSAFLYSGVPY 60
Db 15 DIOMTQSPSSLSASVGDVVTTCRASQIGNDLGMYOQKPKAKRLIYAASSISQSGVPS 74
Oy 61 RFSGSGSGTDFLTITSSLOPEDFATYTCQOQYNIPLTFGOGTKVEIK 107
Db 75 RFSGSGSGTDFLTITSSLOPEDFATYTCQOQYNIPLTFGOGTKVEIK 121

RESULT 8
S46371
Ig kappa chain V-J region (T24-3) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 27-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
C:Accession: S46371; S38645
R:Bensimon, C.; Chastagner, P.; Zouali, M.
EMBO J. 13, 2951-2962, 1994
A:Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene ree
A:Reference number: S46369; MUID:94313975; PMID:8039491
A:Accession: S46371
A:Molecule type: mRNA
A:Residues: 1-117 <BEN>
A:Cross-references: EMBL:Z27172; NID:9415959; PIDN:CAA81696.1; PID:9415960
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:23-97/Domain: immunoglobulin homology <IMM>

Query Match 81.8%; Score 457; DB 2; Length 117;
Best Local Similarity 81.7%; Pred. No. 1.3e-32;
Matches 89; Conservative 9; Mismatches 9; Indels 2; Gaps 1;

Oy 1 DIOMTQSPSSLSASVGDVVTTCRASQNVGTNVMYQOKPKAKRLIYSAFLYSGVPY 60
Db 8 DIOMTQSPSSLSASVGDVVTTCRASQISSTWLMYQOKPKAKRLIYKASTLESQVPS 67
Oy 61 RFSGSGSGTDFLTITSSLOPEDFATYTCQOQYNIPLTFGOGTKVEIK 107
Db 68 RFSGSGSGTDFLTITSSLOPEDFATYTCQOQYNIPLTFGOGTKVEIK 116

RESULT 9
S36264
Ig lambda chain V region (clone alpha-CEA4-8A) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C:Accession: S36264
R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty,
EMBO J. 12, 725-734, 1993
A:Title: Human anti-self antibodies with high specificity from phage display library
A:Reference number: S36256; MUID:93178448; PMID:7679990
A:Accession: S36264
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-107 <GR>
A:Cross-references: EMBL:Z18845; NID:933426; PIDN:CAA79297.1; PID:9339919
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 81.2%; Score 454; DB 2; Length 107;
Best Local Similarity 81.3%; Pred. No. 2.1e-32;
Matches 87; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

Oy 1 DIOMTQSPSSLSASVGDVVTTCRASQNVGTNVMYQOKPKAKRLIYSAFLYSGVPY 60
Db 1 EIVLTQSPSSLSASVGDVVTTCRASQISSTLWYQOKPKAKRLIYAASSISQSGVPS 60
Oy 61 RFSGSGSGTDFLTITSSLOPEDFATYTCQOQYNIPLTFGOGTKVEIK 107
Db 61 RFSGSGSGTDFLTITSSLOPEDFATYTCQOQYNIPLTFGOGTKVEIK 107

RESULT 10
S40331
Ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40331
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40331
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-123 <KLE>
A:Cross-references: EMBL:X72441; NID:9441350; PIDN:CAA51109.1; PID:9441351
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:32-106/Domain: immunoglobulin homology <IMM>

Query Match 80.9%; Score 452; DB 2; Length 123;
Best Local Similarity 83.2%; Pred. No. 3.6e-32;
Matches 89; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

Oy 1 DIOMTQSPSSLSASVGDVVTTCRASQNVGTNVMYQOKPKAKRLIYSAFLYSGVPY 60
Db 17 DIOMTQSPSSLSASVGDVVTTCRASQISSTLWYQOKPKAKRLIYAASSISQSGVPS 76
Oy 61 RFSGSGSGTDFLTITSSLOPEDFATYTCQOQYNIPLTFGOGTKVEIK 107
Db 77 RFSGSGSGTDFLTITSSLOPEDFATYTCQOQYNIPLTFGOGTKVEIK 123

RESULT 11
B49047
Ig kappa chain V region (monoclonal striational autoantibody StrAB SA-1A) - human (fr
C:Species: Homo sapiens (man)
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: B49047
R:Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.
Eur. J. Immunol. 22, 2231-2236, 1992
A:Title: Human monoclonal striational autoantibodies isolated from thymic B lymphocyte
A:Reference number: A49047; MUID:92387224; PMID:1516616
A:Accession: B49047
A:Status: preliminary
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Query Match	80.5%	Score 450;	DB 2:	Length 132;
Best Local Similarity	79.4%;	Pred. No.	5.7e-32;	
Matches	85;	Conservative	10;	Mismatches 12; Indels 0; Gaps 0;
QY	1	DIDMTPSSLSASGDRYTICTKASONGTNAVWVQOKPGAKRALIYSASELTSQVPY	60	
		: : :		
Db	22	DIDLQSPSEFLSASIGDRYTICTRASOGINSTLAWIQOKPGAPKULLIYVASTLOSQVPS	81	
QY	61	RFSGGSGGTDFLTITSLQPEDFAFYCCQAVNYIVLTEGQGKVEIK	107	
		:		
Db	82	RFSGGSGGTETFLTITSLQPEDFAFYCCQFNFSYFTFGGKRVETR	126	

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Search completed: April  2, 2003, 14:40:01
Job time : 44 secs
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GenCore version 5.1.4.D5_4578
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OM protein - protein search, using sw model

Run on: April 2, 2003, 14:28:14 ; Search time 24 Seconds

(without alignments)
184.915 Million cell updates/sec

Title: US-09-875-221B-9

Perfect score: 559
Sequence: 1 DIQMTQSPSSLSASVGRVT.....COQYNIPYLFTEGQTRVEIK 107

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SWISSProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	462	82.6	108	1 KY1V_HUMAN	P04430 homo sapien
2	450	80.5	108	1 KY1H_HUMAN	P01600 homo sapien
3	446	79.8	108	1 KY1G_HUMAN	P01599 homo sapien
4	445	79.6	108	1 KY1R_HUMAN	P01610 homo sapien
5	442	79.1	108	1 KY1M_HUMAN	P01605 homo sapien
6	440	78.7	107	1 KY1F_HUMAN	P01598 homo sapien
7	439.5	78.6	107	1 KY1D_HUMAN	P01596 homo sapien
8	439	78.5	108	1 KY1B_HUMAN	P01594 homo sapien
9	434	77.6	108	1 KY1A_HUMAN	P01604 homo sapien
10	432	77.3	108	1 KY1L_HUMAN	P01608 homo sapien
11	429	76.7	108	1 KY1S_HUMAN	P01611 homo sapien
12	427	76.4	108	1 KY1Q_HUMAN	P01607 homo sapien
13	425	76.0	108	1 KY1O_HUMAN	P01609 homo sapien
14	423	75.7	129	1 KY1C_HUMAN	P04431 homo sapien
15	423	75.1	108	1 KY1G_HUMAN	P01595 homo sapien
16	420	75.1	108	1 KY1A_HUMAN	P01603 homo sapien
17	419	75.0	108	1 KY1A_HUMAN	P01593 homo sapien
18	418	74.8	108	1 KY1E_HUMAN	P01597 homo sapien
19	416	74.4	117	1 KY1I_HUMAN	P01601 homo sapien
20	416	74.4	108	1 KY1N_HUMAN	P01602 homo sapien
21	415	74.2	117	1 KY1J_HUMAN	P01602 homo sapien
22	409	73.2	117	1 KY1J_HUMAN	P04432 homo sapien
23	402	71.9	129	1 KY1X_HUMAN	P04433 homo sapien
24	398	71.2	149	1 KY5A_MOUSE	P01633 mus musculu
25	387.5	69.3	109	1 KY1T_HUMAN	P01612 homo sapien
26	387	69.2	112	1 KY1U_HUMAN	P01613 homo sapien
27	386	69.1	108	1 KY5J_MOUSE	P01643 mus musculu
28	385.5	69.0	129	1 KY3H_HUMAN	P04207 homo sapien
29	384.5	68.8	129	1 KY3L_HUMAN	P18135 homo sapien
30	382	68.3	108	1 KY5Q_MOUSE	P01650 mus musculu
31	381	68.2	108	1 KY5T_MOUSE	P01653 mus musculu
32	381	68.2	128	1 KY5E_MOUSE	P01637 mus musculu
33	379	67.8	108	1 KY5S_MOUSE	P01652 mus musculu

34	378.5	67.7	109	1 KY3D_HUMAN	P01622 homo sapien
35	377.5	67.5	129	1 KY3M_HUMAN	P18136 homo sapien
36	377	67.4	108	1 KY3D_MOUSE	P01636 mus musculu
37	376	67.3	134	1 KY4C_HUMAN	P06314 homo sapien
38	375.5	67.2	109	1 KY3E_HUMAN	P01624 homo sapien
39	373.5	66.8	109	1 KY3E_HUMAN	P01624 homo sapien
40	373	66.7	108	1 KY5E_MOUSE	P01649 mus musculu
41	372	66.5	114	1 KY4A_HUMAN	P01625 homo sapien
42	372	66.5	136	1 KY5B_MOUSE	P01634 mus musculu
43	371	66.4	108	1 KY5L_MOUSE	P01645 mus musculu
44	371	66.4	108	1 KY5R_MOUSE	P01651 mus musculu
45	370.5	66.3	109	1 KY3E_HUMAN	P01623 homo sapien

ALIGNMENTS

RESULT 1				
ID	KY1V_HUMAN	STANDARD:	PRT:	108 AA.
AC	P04430:			
DT	13-AUG-1987 (Rel. 05, Created)			
DT	13-AUG-1987 (Rel. 05, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Ig kappa chain V-I region BAN.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
ON	[1]			
RP	SEQUENCE.			
RX	MEDLINE=86174817; PubMed=3083240;			
RA	Dwulet F.E., O'Connor T.P., Benson M.D.;			
RT	"Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";			
RI	MOL. Immunol. 23:73-78(1986).			
DR	PIR; A01878; K1HUBN.			
DR	HSSP; P80362; 1MTL.			
DR	InterPro: IPR003006; Ig_MHC.			
DR	InterPro: IPR003596; Ig_v.			
DR	Pfam: PF00047; Ig_1.			
DR	SMART; SM00406; IgV_1.			
KW	Immunoglobulin V region; Amyloid.			
FT	DOMAIN 1 24 34			FRAMEWORK-1.
FT	DOMAIN 24 34			COMPLEMENTARITY-DETERMINING-1.
FT	DOMAIN 35 49			FRAMEWORK-2.
FT	DOMAIN 50 56			COMPLEMENTARITY-DETERMINING-2.
FT	DOMAIN 57 88			FRAMEWORK-3.
FT	DOMAIN 89 97			COMPLEMENTARITY-DETERMINING-3.
FT	DOMAIN 98 107			FRAMEWORK-4.
FT	DISULFID 23 88			BY SIMILARITY.
FT	NON_TER 108 108			
SQ	SEQUENCE 108 AA: 11840 MW: CD3FD944FE96FD37 CRC64;			
Query Match 82.6%; Score 462; DB 1; Length 108;				
Best Local Similarity 83.2%; Pred. No. 1.4e-41;				
Matches 89; Conservative 7; Mismatches 11; Indels 0; Gaps 0;				
QY	1 DIQMTQSPSSLSASVGRVTITCKASQNYGVNAMYQQRKAPKALITSASFLYSGVY 60			
DB	1 DIQMTQSPSSLSASVGRVTITCKASQSYNYVAMFQQRKAPKALITSASFLYSGVPS 60			
QY	61 RFSGSGGTDFLTITSLQPEDFATYYCOQYNIPYLFTEGQTRVEIK 107			
DB	61 NRTGSGGTDFLTITSLQPEDFATYYCOQYNIPYLFTEGQTRVQIK 107			
RESULT 2				
ID	KY1H_HUMAN	STANDARD:	PRT:	108 AA.
AC	P01600:			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			

DE Ig kappa chain V-I region Hau.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=71032830; PubMed=4097974;
RA Watanabe S., Hilschmann N.;
RT "The primary structure of a monoclonal kappa-type immunoglobulin L-
chain of subgroup I (Bence-Jones Protein Hau): subdivision within
subgroups.";
RL Hoppe-Sevler's Z. Physiol. Chem. 351:1291-1295(1970).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
DR PIR: A01868; KIHUHU.
DR HSSP: P80362; 1WTL.
DR InterPro: IPR003596; Ig_MHC.
DR Pfam: PF00047; Ig_V.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11671 MW; 08D3A61608D0618 CRC64;

Query Match 80.5%; Score 450; DB 1; Length 108;
Best Local Similarity 81.3%; Pred. No. 2.4e-40;
Matches 87; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIOMTQSPSSLSASVGDRTVITTCASQNVGTNNVAWQKRGKAPKALITYASFLYSGVPY 60
DB 1 DIOMTQSPSSLSASVGDRTVITTCASQNVGTNNVAWQKRGKAPKALITYASFLYSGVPY 60
DB 61 RFGSGSGGTDFTLTISLQPEDPATYCCOQYNYPLTFGCGTVEIK 107
DB 61 RFGSGSGGTDFTLTISLQPEDPATYCCOQYNYPLTFGCGTVEIK 107

RESULT 3
KVIG_HUMAN
ID KVIG_HUMAN STANDARD; PRT; 108 AA.
AC P01599;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region GAL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=75059122; PubMed=4215718;
RA Laure C.J., Watanabe S., Hilschmann N.;
RT "The primary structure of a monoclonal Igm-immunoglobulin
(macroglobulin Gal.), I. The amino acid sequence of the L-chain of
kappa-type, subgroup I.";
RL Hoppe-Sevler's Z. Physiol. Chem. 354:1503-1504(1973).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
DR PIR: A01867; KIHUHL.
DR HSSP: P01607; IREI.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.

DR Pfam: PF00047; Ig_V.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11814 MW; C1AD3CB0F600FE73 CRC64;

Query Match 79.8%; Score 446; DB 1; Length 108;
Best Local Similarity 80.4%; Pred. No. 6.4e-40;
Matches 86; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIOMTQSPSSLSASVGDRTVITTCASQNVGTNNVAWQKRGKAPKALITYASFLYSGVPY 60
DB 1 DIOMTQSPSSLSASVGDRTVITTCASQNVGTNNVAWQKRGKAPKALITYASFLYSGVPY 60
DB 61 RFGSGSGGTDFTLTISLQPEDPATYCCOQYNYPLTFGCGTVEIK 107
DB 61 RFGSGSGGTDFTLTISLQPEDPATYCCOQYNYPLTFGCGTVEIK 107

RESULT 4
KVIR_HUMAN
ID KVIR_HUMAN STANDARD; PRT; 108 AA.
AC P01610;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region WEA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=83273707; PubMed=6410398;
RA Goni F., Frangione B.;
RT "Amino acid sequence of the Fv region of a human monoclonal Igm
(protein WEA) with antibody activity against 3,4-pyruvylated
galactose in Klebsiella polysaccharides K30 and K33.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
WALDENSTROM'S MACROGLOBULINEMIA.
DR PIR: A01876; KIHUWE.
DR HSSP: P80362; 1WTL.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_V.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region; Monoclonal antibody.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11840 MW; 9249B61F0945618C CRC64;

Query Match 79.6%; Score 445; DB 1; Length 108;
Best Local Similarity 78.5%; Pred. No. 8.2e-40;
Matches 84; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIOMTQSPSSLSASVGDRTVITTCASQNVGTNNVAWQKRGKAPKALITYASFLYSGVPY 60

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Db 1 DIOMTQSPSSLSASVGDVRYITICRASQGIKIRNDLTWYQOKPGKAPKRLIYGATSIQSGVPS 60
OY 61 RSSGSGSGTDFLTITSSLOPEDFATYCCQYNYIPLTFEGQTKVEIK 107
DB 61 RSSGSGSGTDFLTITSSLOPEDFATYCCQYNYIPLTFEGQTKVEIK 107

RESULT 5
KV1D_HUMAN
ID KV1D_HUMAN STANDARD: PRT; 108 AA.
AC P01605;
RT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Lay.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=77038198; PubMed=824717;
RA Capra J.D., Klapper D.G.;
RT "Complete amino acid sequence of the variable domains of two human
RT Igm anti-gamma globulins (Lay/Pom) with shared idiotypic
RT specificities.";
RL Scand. J. Immunol. 5:677-684(1976).
CC -1- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS
CC CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POW-V-III KAPPA CHAIN,
CC WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
DR PIR: A01871; KIHULY.
DR HSSP: P01607; 1RET.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT 24 34 COMPLEMENTARITY-DETERMINING-1.
FT 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT 98 107 FRAMEWORK-4.
FT DOMAIN 108 108 BY SIMILARITY.
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11834 MW; 739993A95431434A CRC64;

Query Match 79.1%; Score 442; DB 1; Length 108;
Best Local Similarity 80.4%; Pred. No. 1.7e-39;
Matches 86; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

OY 1 DIOMTQSPSSLSASVGDVRYITICRASQNGTNVAMYQOKPGKAPKRLIYSASFISGVY 60
DB 1 DIOMTQSPSSLSASVGDVRYITICRASQNGTNVAMYQOKPGKAPKRLIYGASTREGVYS 60
OY 61 RSSGSGSGTDFLTITSSLOPEDFATYCCQYNYIPLTFEGQTKVEIK 107
DB 61 RSSGSGSGTDFLTITSSLOPEDFATYCCQYNYIPLTFEGQTKVEIK 107

RESULT 6
KV1F_HUMAN
ID KV1F_HUMAN STANDARD: PRT; 108 AA.
AC P01598;
RT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region EU.
OS Homo sapiens (Human).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=71064023; PubMed=5489770;
RA Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VI. Amino
RT acid sequence of the light chain.";
RL Biochemistry 9:3155-3161(1970).
RN [2]
RP DISULFIDE BOND.
RX MEDLINE=71064027; PubMed=4923144;
RA Gali W.E., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X.
RT Intrachain disulfide bonds.";
RL Biochemistry 9:3188-3196(1970).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR: A01866; KIHBU.
DR HSSP: P01607; 1RET.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT 24 34 COMPLEMENTARITY-DETERMINING-1.
FT 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT 98 107 FRAMEWORK-4.
FT DOMAIN 108 108
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11788 MW; 9CD294F2F4D88823 CRC64;

Query Match 78.7%; Score 440; DB 1; Length 108;
Best Local Similarity 79.4%; Pred. No. 2.7e-39;
Matches 85; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

OY 1 DIOMTQSPSSLSASVGDVRYITICRASQNGTNVAMYQOKPGKAPKRLIYSASFISGVY 60
DB 1 DIOMTQSPSSLSASVGDVRYITICRASQNGTNVAMYQOKPGKAPKRLIYKASSLESQVPS 60
OY 61 RSSGSGSGTDFLTITSSLOPEDFATYCCQYNYIPLTFEGQTKVEIK 107
DB 61 RSSGSGSGTDFLTITSSLOPEDFATYCCQYNSDKMFGQTKVEIK 107

RESULT 7
KV1D_HUMAN
ID KV1D_HUMAN STANDARD: PRT; 107 AA.
AC P01596;
RT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region CAR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=75075135; PubMed=4216454;
RA Milstein C.P., Deverson E.V.;
RT "Primary structure of kappa light chain from a human myeloma
RT protein.";
RL Eur. J. Biochem. 49:377-391(1974).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC MARKER.
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR: A01864; KIHUAR.

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DR HSSP: P80362; 1MTL.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 KW Immunoglobulin V region; Glycoprotein.
 FT CARBOHYD 28 28 N-LINKED (GLCNAC. . .).
 FT NON_TER 107 107
 SQ SEQUENCE 107 AA; 11703 MW; 11BPDP9844C3346 CRC64;

Query Match 78.6%; Score 439.5; DB 1; Length 107;
 Best Local Similarity 78.5%; Pred. No. 3e-39;
 Matches 84; Conservative 11; Mismatches 11; Indels 1; Gaps 1;

QY 1 DIQMTSPSSLSASVGDRTYITCKASQNGTNAVYQOKPGKAPKALISASFLYSGVPY 60
 DB 1 DIQMTSPSSLSASVGDRTYITCKASQNGTNAVYQOKPGKAPKALISASFLYSGVP 60
 QY 61 RFGSGSGTDFLTITSLQPEDPATYCCOYNYIPLTFGGGTVEIK 107
 DB 61 RFGSGSGTDFLTITSLQPEDPATYCCOYNYIPLTFGGGTVEIK 106

RESULT 8

KV1B_HUMAN STANDARD; PRT; 108 AA.
 AC P80362;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region MAT.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP MEDLINE-95086080; PubMed-7993911;
 RA Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M.,
 RA Solomon A., Stevens F.J., Schiffer M.;
 RT "Comparison of crystal structures of two homologous proteins:
 RT structural orders of altered domain interactions in immunoglobulin
 RT light-chain dimers."
 RT Biochemistry 33:14848-14857(1994).
 RN [2]
 RP SEQUENCE OF 1-35.
 RX MEDLINE-8167384; PubMed-6167731;
 RA Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,
 RA Popp R.A., Solomon A.;
 RT "Characterization and preliminary crystallographic data on the VL-
 RT related fragment of the human kappa Bence Jones protein Mat.";
 RT J. Mol. Biol. 147:185-193(1981).
 CC -1- MISCELLANEOUS: THIS IS A BENICE-JONES PROTEIN.
 DR PDB: 1MTL; 01-NOV-94.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; IGV; 1.
 DR SMART: SM00406; IGV; 1.
 KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 107 107 FRAMEWORK-4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT CONFLICT 30 31 TN -> SD (IN REF. 2).
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11737 MW; D9D941B3F0FAE97 CRC64;

Query Match 78.5%; Score 439; DB 1; Length 108;
 Best Local Similarity 78.5%; Pred. No. 3.5e-39;

Matches 84; Conservative 9; Mismatches 14; Indels 0; Gaps 0;

QY 1 DIQMTSPSSLSASVGDRTYITCKASQNGTNAVYQOKPGKAPKALISASFLYSGVPY 60
 DB 1 DIQMTSPSSLSASVGDRTYITCKASQNGTNAVYQOKPGKAPKALISASFLYSGVP 60
 QY 61 RFGSGSGTDFLTITSLQPEDPATYCCOYNYIPLTFGGGTVEIK 107
 DB 61 RFGSGSGTDFLTITSLQPEDPATYCCOYNYIPLTFGGGTVEIK 107

RESULT 9

KV1B_HUMAN STANDARD; PRT; 108 AA.
 AC P01594;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region AU.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE-72189444; PubMed-5028201;
 RA Schlecht H., Hilschmann N.;
 RT "Rule of antibody structure. The primary structure of a monoclonal
 RT immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
 RT protein Au)."
 RT Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY.
 RX MEDLINE-77022433; PubMed-1234024;
 RA Felhammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
 RA Schwager P., Steigemann W., Schramm H.J.;
 RT "The structure determination of the variable portion of the
 RT Bence-Jones protein Au."
 RT Biophys. Struct. Mech. 1:139-146(1975).
 CC -1- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY
 CC MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V
 CC REGION OF THE KAPPA CHAIN REI.
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -1- MISCELLANEOUS: THIS IS A BENICE-JONES PROTEIN.
 DR PIR: A01862; K1HNU.
 DR HSSP: P01607; IRET.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; IGV; 1.
 DR SMART: SM00406; IGV; 1.
 KW Immunoglobulin V region; Bence-Jones protein.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 FRAMEWORK-4.
 FT DOMAIN 107 107 COMPLEMENTARITY-DETERMINING-3.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11939 MW; E8011187E66FB9 CRC64;

Query Match 77.6%; Score 434; DB 1; Length 108;
 Best Local Similarity 79.4%; Pred. No. 1.2e-38;
 Matches 85; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

QY 1 DIQMTSPSSLSASVGDRTYITCKASQNGTNAVYQOKPGKAPKALISASFLYSGVPY 60
 DB 1 DIQMTSPSSLSASVGDRTYITCKASQNGTNAVYQOKPGKAPKALISASFLYSGVP 60
 QY 61 RFGSGSGTDFLTITSLQPEDPATYCCOYNYIPLTFGGGTVEIK 107
 DB 61 RFGSGSGTDFLTITSLQPEDPATYCCOYNYIPLTFGGGTVEIK 107

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RESULT 10
KYL_HUMAN
ID KYL_HUMAN STANDARD: PRT; 108 AA.
AC P01604;
DR 21-JUL-1986 (Rel. 01, Created)
DR 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=79237924; PubMed=112021;
RA Eultz M., Kley H.-P., Zeltner H.-J.;
RT "The primary structure of the Bence-Jones protein Kue. The amino acid
RL sequence of the variable part of a human L-chain of the kappa-type.";
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR: A01870; KIHUKU.
DR HSSP: P01607; IREI.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 2 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 3 35 49 FRAMEWORK-2.
FT DOMAIN 4 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 5 57 88 FRAMEWORK-3.
FT DOMAIN 6 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 7 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 12127 MW; 906679A5D90E4E98 CRC64;

Query Match 77.3%; Score 432; DB 1; Length 108;
Best Local Similarity 76.6%; Pred. No. 1.9e-38;
Matches 82; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIQMTPSSSLASVGDRTITCKASQNGTVAMVYQKPKAPKALIIYSASFLYSGVY 60
DB 1 DIQMTPSSSLASVGDRTITCKASQNGTVAMVYQKPKAPKALIIYSASFLYSGVY 60
QY 61 RFSGSGSGTDFLTITSSLOPEPATYCCOQYNYNPLTFGQTKVEIK 107
DB 61 RFSGSGSGTDFLTITSSLOPEPATYCCOQYNYNPLTFGQTKVEIK 107

RESULT 11
KYL_HUMAN
ID KYL_HUMAN STANDARD: PRT; 108 AA.
AC P01608;
DR 21-JUL-1986 (Rel. 01, Created)
DR 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=68362076; PubMed=5595110;
RA Hilschmann N.;
RT "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and
RT Cum.)";
RL Hope-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).

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RN [2]
RP REVISIONS TO 39 AND 41.
RA Hilschmann N., Barnakol H.U., Hess M., Langer B., Ponstingl H.,
RA Steinmetz-Kayne M., Suter L., Watanabe S.;
RL (in) Franek F., Shugar D. (eds.);
RL Gamma globulins: structure and function, pp.57-74, Academic Press,
RL New York (1969).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR: A01874; KIHURY.
DR HSSP: P80362; IWTU.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 2 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 3 35 49 FRAMEWORK-2.
FT DOMAIN 4 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 5 57 88 FRAMEWORK-3.
FT DOMAIN 6 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 7 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11782 MW; F5ACED5A313DF3A CRC64;

Query Match 76.7%; Score 429; DB 1; Length 108;
Best Local Similarity 77.6%; Pred. No. 3.8e-38;
Matches 83; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 1 DIQMTPSSSLASVGDRTITCKASQNGTVAMVYQKPKAPKALIIYSASFLYSGVY 60
DB 1 DIQMTPSSSLASVGDRTITCKASQNGTVAMVYQKPKAPKALIIYSASFLYSGVY 60
QY 61 RFSGSGSGTDFLTITSSLOPEPATYCCOQYNYNPLTFGQTKVEIK 107
DB 61 RFSGSGSGTDFLTITSSLOPEPATYCCOQYNYNPLTFGQTKVEIK 107

RESULT 12
KYL_HUMAN
ID KYL_HUMAN STANDARD: PRT; 108 AA.
AC P01611;
DR 21-JUL-1986 (Rel. 01, Created)
DR 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=81092279; PubMed=6778806;
RA Kratzin H., Tang C., Kirsche J.U., Hilschmann N.;
RT "Preparative separation of the tryptic hydrolysate of a protein by
RT high-pressure liquid chromatography. The primary structure of a
RT monoclonal L-chain of k-type, subgroup I (Bence-Jones Protein
RT Wes).";
RL Hope-Seyler's Z. Physiol. Chem. 361:1591-1598(1980).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR: A01877; KIHUWS.
DR HSSP: P80362; IWTU.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 24 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 2 34 FRAMEWORK-1.

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FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11608 MW; 782B14A649A60845 CRC64;

Query Match 76.4%; Score 427; DB 1; Length 108;
Best Local Similarity 78.5%; Pred. No. 6.2e-38;
Matches 84; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIQMTGSPSSLSASVGRVITTCASQNGVTNVAWYQKRGKAPKALITYSASFYSGVPY 60
DB 1 DIQMTGSPSSLSASVGRVITTCASQNGVTNVAWYQKRGKAPKALITYSASFYSGVPY 60
DB 61 RFGSGSGTDFTLTISLOPEDFATYCCQYNYPLTFEGGTVEIK 107
QY 61 RFGSGSGTDFTLTISLOPEDFATYCCQYNYPLTFEGGTVEIK 107
DB 61 RFGSGSGTDFTLTISLOPEDFATYCCQYNYPLTFEGGTVEIK 107

RESULT 13
KV10_HUMAN STANDARD; PRT; 108 AA.
AC P01609;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Scw.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=75059271; PubMed=4435756;
RA Eulitz M., Hilschmann N.;
RT "The primary structure of a human immunoglobulin L-chain of
RT kappa-type (Bence-Jones protein Scw.); II: The chymotryptic peptides
RT and the complete amino acid sequence."
RL Hoppe-Seyler's Z. Physiol. Chem. 355:842-866(1974).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A01875; KIHUSW.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11764 MW; 32CECDDDF9644414 CRC64;

Query Match 76.0%; Score 425; DB 1; Length 108;
Best Local Similarity 75.7%; Pred. No. 1e-37;
Matches 81; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 1 DIQMTGSPSSLSASVGRVITTCASQNGVTNVAWYQKRGKAPKALITYSASFYSGVPY 60
DB 1 DIQMTGSPSSLSASVGRVITTCASQNGVTNVAWYQKRGKAPKALITYSASFYSGVPY 60
QY 61 RFGSGSGTDFTLTISLOPEDFATYCCQYNYPLTFEGGTVEIK 107
DB 61 RFGSGSGTDFTLTISLOPEDFATYCCQYNYPLTFEGGTVEIK 107
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DB 61 RFGSGSGTDFTLTISLOPEDIGNYCCQYDNVPITFGGTVEIK 107
RESULT 14
KV10_HUMAN STANDARD; PRT; 108 AA.
AC P01607;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Rel.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76023758; PubMed=809329;
RA Palm W., Hilschmann N.;
RT "The primary structure of a crystalline monoclonal immunoglobulin
RT kappa-type L-chain, subgroup I (Bence-Jones protein Rel.); Isolation
RT and characterization of the tryptic peptides; the complete amino acid
RT sequence of the protein; a contribution to the elucidation of the
RT three-dimensional structure of antibodies, in particular their
RT combining site."
RL Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=7603968; PubMed=1182131;
RA Epp O., Latman E.E., Schiffer M., Huber R., Palm W.;
RT "The molecular structure of a dimer composed of the variable portions
RT of the Bence-Jones protein REI refined at 2.0-A resolution."
RL Biochemistry 14:4943-4952(1975).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A01873; KIHURE.
DR PDB; IREI; 17-FEB-84.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 23 88 FRAMEWORK-4.
FT STRAND 2 7
FT STRAND 4 13
FT STRAND 10 16
FT STRAND 15 25
FT STRAND 19 31
FT STRAND 30 38
FT STRAND 40 41
FT STRAND 45 49
FT STRAND 50 52
FT STRAND 53 54
FT STRAND 55 57
FT STRAND 56 61
FT STRAND 62 69
FT STRAND 68 67
FT STRAND 70 75
FT STRAND 80 82
FT STRAND 85 90
FT STRAND 98 98
FT STRAND 102 106
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11902 MW; 9E8143E118BCE2A CRC64;
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Search completed: April  2, 2003, 14:37:38
Job time : 25 secs
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Query Match	75.7%;	Score 423;	DB 1;	Length 108;
Best Local Similarity	77.4%;	Pred. No. 1.6e-37;		
Matches 82;	Conservative 8;	Mismatches 16;	Indels 0;	Gaps 0;

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GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: April 2, 2003, 14:33:54 ; Search time 86 Seconds
(without alignments)
256.361 Million cell updates/sec

Title: US-09-875-221b-9

Perfect score: 559

Sequence: 1 DIQMTPSSLSASVGDRTV.....CQGYNYPLTFGGTKVEIK 107

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL_21:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rviro:*

16: sp_bacteriap:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	451	80.7	108	4 Q9UL70	Q9UL70 homo sapien
2	448	80.1	108	11 Q8VJF0	Q8VJF0 mus musculu
3	438.5	78.4	107	4 Q96SA9	Q96SA9 homo sapien
4	436	78.0	108	4 Q9UL77	Q9UL77 homo sapien
5	427	76.4	108	4 Q9UL79	Q9UL79 homo sapien
6	416	74.4	116	4 Q96PF6	Q96PF6 homo sapien
7	415.5	74.3	107	4 Q9UL81	Q9UL81 homo sapien
8	394	70.5	108	4 Q9UL83	Q9UL83 homo sapien
9	387.5	69.3	109	4 Q9UL85	Q9UL85 homo sapien
10	385	68.9	214	11 Q9RIAS	Q9RIAS mus musculu
11	383	68.5	214	11 Q8R062	Q8R062 mus musculu
12	379	67.8	233	11 Q9LWS9	Q9LWS9 mus musculu
13	376	67.3	234	11 Q8VCP0	Q8VCP0 mus musculu
14	374.5	67.0	109	4 Q9UL78	Q9UL78 homo sapien
15	373	66.7	109	11 Q920E6	Q920E6 mus musculu
16	369	66.0	234	11 Q9LWF8	Q9LWF8 mus musculu

17	369	66.0	298	11 Q9GYF0	Q9GYF0 mus musculu
18	367	65.7	107	11 Q9JL84	Q9JL84 mus musculu
19	357	63.9	127	11 Q925S9	Q925S9 mus musculu
20	348.5	62.3	109	4 Q9UL86	Q9UL86 homo sapien
21	344	61.5	111	11 Q920E9	Q920E9 mus musculu
22	338	60.5	99	11 Q9JL74	Q9JL74 mus musculu
23	337.5	60.4	106	5 Q9UL10	Q9UL10 schistosoma
24	334.5	59.8	241	11 Q921A6	Q921A6 mus musculu
25	332.5	59.5	134	11 Q8VDD0	Q8VDD0 mus musculu
26	329	58.9	107	11 Q9ER29	Q9ER29 mus musculu
27	320.5	57.3	238	11 Q99M37	Q99M37 mus musculu
28	318.5	57.0	235	11 Q9JL12	Q9JL12 mus musculu
29	313.5	56.1	238	11 Q8VCI6	Q8VCI6 mus musculu
30	304.5	54.5	239	11 Q8VC55	Q8VC55 mus musculu
31	301	53.8	101	11 Q9JL78	Q9JL78 mus musculu
32	300	53.7	97	11 Q9JL76	Q9JL76 mus musculu
33	300	53.7	103	11 Q9JL80	Q9JL80 mus musculu
34	297.5	53.2	239	4 Q8TCD0	Q8TCD0 homo sapien
35	289	51.7	109	6 Q9N0M5	Q9N0M5 oryctolagus
36	289	51.7	114	4 Q9UL80	Q9UL80 homo sapien
37	289	51.7	234	11 Q8R028	Q8R028 mus musculu
38	287.5	51.4	104	11 Q9JL82	Q9JL82 mus musculu
39	248.5	44.5	237	4 Q8WT06	Q8WT06 homo sapien
40	242.5	43.4	237	4 Q8WUR4	Q8WUR4 homo sapien
41	234.5	41.9	236	4 Q96E61	Q96E61 homo sapien
42	231.5	41.4	110	4 Q8TE63	Q8TE63 homo sapien
43	221.5	39.6	108	4 Q96S80	Q96S80 homo sapien
44	219.5	39.3	233	4 Q8TBC9	Q8TBC9 homo sapien
45	217.5	38.9	112	4 Q96JDL	Q96JDL homo sapien

ALIGNMENTS

RESULT 1

ID Q9UL70 PRELIMINARY: PRT; 108 AA.

AC Q9UL70:

DT 01-MAY-2000 (TREMBLrel. 13 Created)

DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)

DE Myosin-reactive immunoglobulin light chain variable region (Fragment).

DE (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98277139; PubMed=9614934;

RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M., Young D.C.;

RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."

RL Clin. Immunol. Immunopathol. 87:184-192(1998).

DR EMBL: AF035044; AAD56280.1; -

DR HSSP: P01607; IPR1.

DR InterPro: IPR003006; IG_MHC.

DR InterPro: IPR003596; IG_V.

DR Pfam: PF00047; IG_1.

DR SMART: SM00406; IGv; 1.

FT NON_TER 1

FT NON_TER 1

SO SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 80.7%; Score 451; DB 4; Length 108;

Best Local Similarity 81.3%; Pred. No. 5.3e-40;

Matches 87; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

Oy 1 DIQMTPSSLSASVGDRTVTTCKASQNVGTVWYQOKPGKAPKALYSASFLYSVPY 60

Db 1 DIQMTPSSLSASVGDRTVTTCKASQNVGTVWYQOKPGKAPKALYSASFLYSVPY 60

OY 61 RFGSGSGTDFLTITSSLOPEDFATYYCOQYNIPYLFEGGTRVEIK 107
 DB 61 RFGSGSGTDFLTITSSLOPEDFATYYCOQYNIPYLFEGGTRVEIK 107

RESULT 2

OBYIJO PRELIMINARY; PRT; 108 AA.

AC 08VIJ0; 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
 DE Anti-DNA light chain (Fragment).
 GN VKI9.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID-10090;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C3H/HEJ-LPR/LPR;
 RX MEDLINE-96409289; PubMed-8814271;
 RA Wlooh M.K., Alexander A.L., Pippen A.M., Pisetsky D.S., Gillespie G.S.;
 RT "Differences in V kappa gene utilization and VH CDR3 sequence among
 RT anti-DNA from C3H/129 mice and lupus mice with nephritis.";
 RL Eur. J. Immunol. 26:2225-2233(1996).
 DR EMBL; U59155; AAB02917.1;
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig: 1.
 DR SMART; SM00409; Ig; 1.
 DR SMART; SM00406; Ig; 1.
 FT NON_TER 1
 FT NON_TER 108
 SQ SEQUENCE 108 AA; 11859 MW; 68506D75613DBFBE CRC64;

Query Match 80.1%; Score 448; DB 11; Length 108;
 Best Local Similarity 77.6%; Pred. No. 1,1e-39;
 Matches 83; Conservative 13; Mismatches 11; Indels 0; Gaps 0;

OY 1 DIQMTSPSSLSASVGDRTITCKASQNGTNVAVYQKPGKAPKALISASFLYSGVPY 60
 DB 1 DIQMTSPSSLSASVGDRTITCKASQNGTNVAVYQKPGKAPKALISASFLYSGVH 60

OY 61 RFGSGSGTDFLTITSSLOPEDFATYYCOQYNIPYLFEGGTRVEIK 107
 DB 61 RFGSGSGTDFLTITSSLOPEDFATYYCOQYNIPYLFEGGTRVEIK 107

RESULT 3
 O96SA9 PRELIMINARY; PRT; 107 AA.

AC 096SA9; 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
 DE Anti-streptococcal/anti-myoisin immunoglobulin kappa light chain
 DE variable region (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominda; Homo.
 OX NCBI_TaxID-9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-98375893; PubMed-9712075;
 RA Adderson E.E., Shikhan A.R., Ward K.E., Cunningham M.W.;
 RT "Molecular analysis of polyclonal monoclonal antibodies from
 RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
 RT antibody V region genes.";
 RL J. Immunol. 161:2020-2031(1998).
 DR EMBL; U96396; AAB68785.1;
 DR InterPro: IPR003006; Ig_MHC.

DR Pfam: PF00047; Ig: 1.
 FT NON_TER 1
 FT NON_TER 107
 SQ SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577E16 CRC64;

Query Match 78.4%; Score 438.5; DB 4; Length 107;
 Best Local Similarity 82.2%; Pred. No. 1,1e-38;
 Matches 88; Conservative 7; Mismatches 11; Indels 1; Gaps 1;

OY 1 DIQMTSPSSLSASVGDRTITCKASQNGTNVAVYQKPGKAPKALISASFLYSGVPY 60
 DB 1 DIQMTSPSSLSASVGDRTITCKASQNGTNVAVYQKPGKAPKALISASFLYSGVPS 60

OY 61 RFGSGSGTDFLTITSSLOPEDFATYYCOQYNIPYLFEGGTRVEIK 107
 DB 61 RFGSGSGTDFLTITSSLOPEDFATYYCOQYNIPYLFEGGTRVEIK 106

RESULT 4

O9UL77 PRELIMINARY; PRT; 108 AA.

AC 09UL77; 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE Myosin-reactive immunoglobulin light chain variable region
 DE (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominda; Homo.
 OX NCBI_TaxID-9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE-98277139; PubMed-9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus.";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035037; AAD56273.1; -.
 DR HSP; P01607; IREI.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig: 1.
 DR SMART; SM00406; Ig; 1.
 FT NON_TER 1
 FT NON_TER 108
 SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 78.0%; Score 436; DB 4; Length 108;
 Best Local Similarity 80.4%; Pred. No. 2e-38;
 Matches 86; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

OY 1 DIQMTSPSSLSASVGDRTITCKASQNGTNVAVYQKPGKAPKALISASFLYSGVPY 60
 DB 1 DIQMTSPSSLSASVGDRTITCKASQNGTNVAVYQKPGKAPKALISASFLYSGVPS 60

OY 61 RFGSGSGTDFLTITSSLOPEDFATYYCOQYNIPYLFEGGTRVEIK 107
 DB 61 RFGSGSGTDFLTITSSLOPEDFATYYCOQYNIPYLFEGGTRVEIK 107

RESULT 5

O9UL79 PRELIMINARY; PRT; 108 AA.

AC 09UL79; 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE Myosin-reactive immunoglobulin light chain variable region
 DE (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=98277139; Pubmed=9614934;
RA	Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RT	Young D.C.;
RT	"W50sh1n-reactive autoantibodies in rheumatic carditis and normal
RT	fetus.";
RL	Clin. Immunol. Immunopathol. 87:184-192(1998).
DR	EMBL; AF035035; AA056271.1; -.
DR	HSSP; P01607; IREI.
DR	InterPro; IPR003006; IG_MHC.
DR	InterPro; IPR003596; IG_v.
DR	Pfam; PF00047; Ig; 1.
DR	SMART; SM00406; IGV; 1.
FT	NON_TER 1
FT	NON_TER 1
Q0	SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;

Query Match	76.48;	Score 427;	DB 4;	Length 108;
Best Local Similarity	77.68;	Pred.No. 1.8e-37;		
Matches 83; Conservative		8; Mismatches 16;	Indels 0;	Gaps 0

[illegible]

ID	Q96PF6	PRELIMINARY:	PRT:	116 AA.
AC	Q96PF6;			
DT	01-DEC-2001 (TREMBlrel, 19, Created)			
DT	01-DEC-2001 (TREMBlrel, 19, Last sequence update)			
DT	01-MAR-2002 (TREMBlrel, 20, Last annotation update)			
DE	Kappa 1 light chain variable region (Fragment).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21361171; PubMed=11468171;			
RA	Comenzo R.L., Zhang Y., Martinez C., Osman K., Herrera G.A.;			
RT	"The tropism of organ involvement in primary systemic amyloidosis			
RT	contributions of Ig V(L) germ line gene use and clonal plasma cel			
RT	burden.";			
RL	Blood 98:714-720(2001).			
DR	EMBL; AF361758; AAK51465.1; -			
DR	InterPro; IPR003006; Ig_MHC.			
DR	Pfam; PF00047; Ig; 1.			
FT	NON_TER	1	1	
FT	NON_TER	116	116	
QO	SEQUENCE	116 AA;	E796FC2217BFCE57 CRC64;	

Query Match	74.48;	Score 416;	DB 4;	length 116;
Best Local Similarity	72.98;	Pred. No. 2.8e-36;		
Matches 78;	Conservative 12;	Mismatches 17;	Indels 0;	Gaps 0;

[illegible]

RESULT 7	ID	PRELIMINARY;	PRT;	107 AA.
090UL81	090UL81			
AC	Q90L81;			
DT	01-MAY-2000 (TrEMBLrel. 13, Created)			
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)			
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)			
DE	Myosin-reactive Immunoglobulin light chain variable region (Fragment).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=98277139; Pubmed=9614934;			
RA	Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,			
RT	Young D.C.;			
RT	"Wysin-reactive autoantibodies in rheumatic carditis and normal			
RT	fetus.";			
RL	Clin. Immunol. Immunopathol. 87:184-192(1998).			
RL	EMBL; AF035033; AAD56659.1; -			
DR	HSSP; P01607; IRET.			
DR	InterPro; IPR003006; Ig_MHC.			
DR	InterPro; IPR003596; Ig_V.			
DR	Pfam; PF00047; Ig_1.			
DR	SMART; SM00406; IGV_1.			
FT	NON_TER			
FT	1			
FT	107			
FT	SEQUENCE			
FT	107 AA; 11501 MW; 070549FDE0754748 CRC64;			

Query Match	74.38;	Score 415.5;	DB 4;	Length 107;
Best Local Similarity	77.68;	Pred. No. 2.8e-36;		
Matches 83; Conservative	8;	Mismatches 15;	Indels 1;	Gaps 1;

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OY 1 DLOMOPSPSSLSASVGDRTVTCRKSQWVGNVMAOQCKKAPKALVYSFLXSPVY 60
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 DLOMOPSPSSLSASVGDRTVTCRKSQWVGNVMAOQCKKAPKALVYSFLXSPVY 60
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 61 RSSGSGSGTDFLTLLTSSLOPEDFATVYCOQYINIXPLTFEGQKVEIK 107
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 RSSGSGSGTDFLTLLTSSLOPEDFATVYCOQYINIXPLTFEGQKVEIK 106
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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RESULT 8	
Q9UL83	
ID	Q9UL83
AC	Q9UL83;
DT	01-MAY-2000 (TREMBLrel. 13, Created)
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE	Myosin-reactive immunoglobulin light chain variable region (Fragment).
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX	NCBI TaxID=9606;

RA	Wu X., Liu B., Van der Meewe P.L., Kais N.N., Berney S.M.,
RA	Young D.C.;
RT	"Wysin-reactive autoantibodies in rheumatic carditis and normal
RT	fetus.";
RL	Clin. Immunol. Immunopathol. 87:184-192(1998).
DR	EMBL: AF035031; AD56267.1; -
DR	HSSP; P80362; 1WTL.
DR	InterPro: IPR003006; Ig_MHC.
DR	InterPro: IPR003596; Ig_v.
DR	Pfam: PF00047; Ig; 1.
DR	SMART: SMO0406; IGV; 1.
FT	NON TER 1 1

```
FT NON_TER 108 108
SQ SEQUENCE 108 AA: 11834 MW: 9F9C5A92EBA96EEA CRC64:

Query Match
Best Local Similarity 70.5%; Score 394; DB 4; Length 108;
Matches 73; Conservative 17; Mismatches 17; Indels 0; Gaps 0;

OY 1 DIOMTQSPSSLSASVGDRTYITCKASQNGTVNAVYQOKPGKAPKALITYSASFYSGVPY 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 EIVMQSPATLSVSPGERATLSCRASQSYSSNLAWYQOKPGQAPRLITYGASTRATGIRA 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

OY 61 RFGSGSGDTFLTITSSLOPEDFATYVCOQYNYIPLTFGQGTKEIK 107
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 RFGSGSGDTFLTITSSLOPEDFATYVCOQYNYIPLTFGQGTKEIK 107
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 9
OY0U85 PRELIMINARY; PRT; 109 AA.
AC O90U85;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Myosin-reactive immunoglobulin kappa chain variable region
   (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-98277139; PubMed-9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Betney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
   fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035029; AAD56265.1; -.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV_1.
FT NON_TER 1 109
FT SEQUENCE 109 AA: 11761 MW: FB1E43E7C7AFACCC CRC64:

Query Match
Best Local Similarity 69.3%; Score 387.5; DB 4; Length 109;
Matches 74; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

OY 1 DIOMTQSPSSLSASVGDRTYITCKASQNGTVNAVYQOKPGKAPKALITYSASFYSGVPY 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 EIVMQSPATLSVSPGERATLSCMASQSYSSNLAWYQOKPGQAPRLITYGASTRATGIRA 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

OY 61 RFGSGSGDTFLTITSSLOPEDFATYVCOQYNYIPLTFGQGTKEIK 107
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 RFGSGSGDTFLTITSSLOPEDFATYVCOQYNYIPLTFGQGTKEIK 107
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 10
OY0U85 PRELIMINARY; PRT; 214 AA.
AC O90U85;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Kappa light chain of Mab7 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
```

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RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.R.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
   antibody (Mab 7, its light and heavy chains) and construction of a
   single chain antibody (scFv).";
RT Submitted (May-1999) to the EMBL/genbank/DBJ databases.
DR EMBL; AF152371; AAD40242.1; -.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR003600; IG_Like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00406; IGV_1.
DR SMART; SM00410; IG_Like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT NON_TER 1 214
FT SEQUENCE 214 AA: 23922 MW: 52BA205FDE95E2A CRC64:

Query Match
Best Local Similarity 68.9%; Score 385; DB 11; Length 214;
Matches 71; Conservative 18; Mismatches 18; Indels 0; Gaps 0;

OY 1 DIOMTQSPSSLSASVGDRTYITCKASQNGTVNAVYQOKPGKAPKALITYSASFYSGVPY 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 DIOMTQSPSSLSASVGDRTYITCKASQNGTVNAVYQOKPGKAPKALITYSASFYSGVPY 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

OY 61 RFGSGSGDTFLTITSSLOPEDFATYVCOQYNYIPLTFGQGTKEIK 107
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 RFGSGSGDTFLTITSSLOPEDFATYVCOQYNYIPLTFGQGTKEIK 107
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 11
OY0R062 PRELIMINARY; PRT; 234 AA.
AC O8R062;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Hypothetical 25.9 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX Strausberg R.;
RT Submitted (Apr-2002) to the EMBL/genbank/DBJ databases.
DR EMBL; BC027418; AAH27418.1; -.
KW Hypothetical protein.
SQ SEQUENCE 234 AA: 25857 MW: 4EB08C81426AEAB1 CRC64:

Query Match
Best Local Similarity 68.5%; Score 383; DB 11; Length 234;
Matches 73; Conservative 13; Mismatches 21; Indels 0; Gaps 0;

OY 1 DIOMTQSPSSLSASVGDRTYITCKASQNGTVNAVYQOKPGKAPKALITYSASFYSGVPY 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 21 DIOMTQSPSSLSASVGDRTYITCKASQNGTVNAVYQOKPGQGTKEIK 80
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

OY 61 RFGSGSGDTFLTITSSLOPEDFATYVCOQYNYIPLTFGQGTKEIK 107
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 81 RFGSGSGDTFLTITSSLOPEDFATYVCOQYNYIPLTFGQGTKEIK 127
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 12
OY1WS9 PRELIMINARY; PRT; 233 AA.
AC O91WS9;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
```

DE Hypothetical 25.8 kDa protein (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=COLON;
 RA Strausberg R.;
 RL Submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL: BC013496; AAH13496.1; -
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; Ig_2.
 DR PROSITE: PS00290; Ig_MHC; UNKNOWN_1.
 KW Hypothetical protein.
 FT NON_TER 1
 SQ SEQUENCE 233 AA; 25781 MW; B1C184DA149A16EB CRC64;

Query Match 67.8%; Score 379; DB 11; Length 233;
 Best Local Similarity 68.2%; Pred. No. 5,2e-32;
 Matches 73; Conservative 11; Mismatches 23; Indels 0; Gaps 0;

OY 1 DIQMTQSPSSLSASVGDRTYITCKASQNVGVAMVYQKPGKAPKALITYSASFLYSGVPY 60
 DB 20 DIQMTQSPSSLSASVGDRTYITCKASQNVGVAMVYQKPGKAPKALITYSASFLYSGVPS 79
 OY 61 RFGSGSGDTFTLTSSLOPEDFATYCCQYNYIPLTFGQTKVEIK 107
 DB 80 RFGSGSGDTFTLTSSLOPEDFATYCCQYNYIPLTFGQTKVEIK 126

RESULT 13

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=COLON;
 RA Strausberg R.;
 RL Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL: BC019474; AAH19474.1; -
 DR InterPro: IPR003599; Ig_2.
 DR InterPro: IPR003597; Ig_C1.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig_2.
 DR SMART: SM00409; Ig_2.
 DR SMART: SM00407; Ig_C1.
 DR PROSITE: PS00290; Ig_MHC; UNKNOWN_1.
 KW Hypothetical protein.
 FT NON_TER 1
 SQ SEQUENCE 234 AA; 25702 MW; 102551C58AC2FA9F CRC64;

Query Match 67.3%; Score 376; DB 11; Length 234;
 Best Local Similarity 65.4%; Pred. No. 1.1e-31;
 Matches 70; Conservative 18; Mismatches 13; Indels 0; Gaps 0;

OY 1 DIQMTQSPSSLSASVGDRTYITCKASQNVGVAMVYQKPGKAPKALITYSASFLYSGVPY 60
 DB 21 DIQMTQSPSSLSASVGEVYITICRASQNVGVAMVYQKPGKAPKALITYSASFLYSGVPS 80
 OY 61 RFGSGSGDTFTLTSSLOPEDFATYCCQYNYIPLTFGQTKVEIK 107
 DB 81 RFGSGSGDTFTLTSSLOPEDFATYCCQYNYIPLTFGQTKVEIK 127

RESULT 14

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus".
 RL Clin. Immunol. Immunopathol. 87:104-192(1998).
 DR EMBL: AF035036; AAD56272.1; -
 DR HSP: P80362; 1MTL.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00406; Ig_1.
 DR NON_TER 1
 FT NON_TER 109
 SQ SEQUENCE 109 AA; 11646 MW; 5F675C52EC7EE197 CRC64;

Query Match 67.0%; Score 374.5; DB 4; Length 109;
 Best Local Similarity 66.7%; Pred. No. 6e-32;
 Matches 72; Conservative 16; Mismatches 19; Indels 1; Gaps 1;

OY 1 DIQMTQSPSSLSASVGDRTYITCKASQNVGVAMVYQKPGKAPKALITYSASFLYSGVPY 59
 DB 1 EIVTQSPGTLSPERATISCRASQVSSSLAVYQKPGKAPKALITYSASFLYSGVPS 60
 OY 60 YRFGSGSGDTFTLTSSLOPEDFATYCCQYNYIPLTFGQTKVEIK 107
 DB 61 DRFGSGSGDTFTLTSSLOPEDFATYCCQYNYIPLTFGQTKVEIK 108

RESULT 15

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC "Definition of the idiotope of Pterin-Mimicking Antibodies Expressed in Mammalian Cells".
 RA Atkin J.D., Jape A., Jennings I.G., Horvath O., Cotton R.G.H.;
 RT Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF030938; AAL09422.1; -
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; Ig_1.
 DR NON_TER 1
 FT NON_TER 109
 SQ SEQUENCE 109 AA; 11943 MW; DAD3F98E05DD1501 CRC64;

Query Match 66.7%; Score 373; DB 11; Length 109;
 Best Local Similarity 66.4%; Pred. No. 8.6e-32;

	Matches	71;	Conservative	15;	Mismatches	21;	Indels	0;	Gaps	0;
OY	1	DIQMTQSPSSLSASVGDRVTITCKASQNVGTNAVYQQRKAPKALITYSASFLYSGVPY	60							
Db	1	DIQMTQSPASLSASVGETVITTCRASGNHNYLAWYQQRKSPOLLVYNAKTLADGVPS	60							
OY	61	RFSGSGSGTDFTLTISSLQPEDFATYYCOQXNYPLTFGGGTVEIK	107							
Db	61	RFSGSGSGTQYSLKINSLSQPEDFGSYCOHFWSTPMTFGGGRLEIK	107							

Search completed: April 2, 2003, 14:39:10
 Job time : 87 secs